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/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pGVN-66124"
/clone_1b="GVN"
/tissue_type="N2-fixing root nodules"
/dev_stage="effective root nodules harvested one month
post inoculation with Sinorhizobium meliloti"

```



Db 509 CAATCAGTTCAATTAAGGCTCAATACGATGCGAAGCAATGCAAGATATTGGGCG 568  
 QY 541 CAAATCGGAAGCAAGCAACTATGCAATGGCAGGCTTCCCTTCAAGCACTCTT 600  
 Db 569 CAAATTTGGCAAGCAATCTTATGATATGGTCAAGTCTTCAATTTATGTCACACA 628  
 QY 601 AGTAGATGCGACATCTCACTGCTTAAATCTGCTTCCCAATTTGGCAATTTGGCAA 660  
 Db 629 AGTAGATGGAAGGAGCACTATTTAGCAACAATGCTGACCAACAATATTGGCAATTTGGACA 688  
 QY 661 ACCTATGAGGCCCTCAATT 680  
 Db 689 ACTTTTGAAGGGGCTCAATT 708  
 RESULT 3  
 AM574064 646 bp mRNA linear EST 07-SEP-2000  
 LOCUS AM574064  
 DEFINITION EST13655 GVN Medicago truncatula cdna clone pgvn-51c8, mRNA  
 sequence.  
 ACCESSION AM574064 GI:7238797  
 VERSION AM574064.1 GI:7238797  
 KEYWORDS EST.  
 SOURCE Medicago truncatula  
 ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;  
 Medicago.  
 1 (bases 1 to 646)  
 REFERENCE  
 AUTHORS Fedorova, M., Pierson, B.L., Samac, D.A., Vance, C.P., Gantt, J.S., Peng  
 H., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S.,  
 Holt, I.E. and Fraser, C.M.  
 TITLES ESTs from one month old nitrogen-fixing root nodules of Medicago  
 truncatula  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Carroll P. Vance  
 Department of Agronomy and Plant Genetics  
 University of Minnesota  
 411 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108 USA  
 Tel: 612 625 5715  
 Fax: 651-649-5058  
 Email: Vance004@maroon.tc.umn.edu  
 Minnesota EST name: M252962e  
 TIGR sequence name: MTCAR16TK  
 More information is available at:  
 'http://chryslr.tamu.edu/medicago/'  
 Seq primer: SKmod (CTA gaa CTA gta gat CC).  
 Location/Qualifiers  
 FEATURES  
 source  
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 /cultivar="genotype A17"  
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 /clone="pgvn-51c8"  
 /clone\_lib="GVN"  
 /tissue\_type="N2-fixing root nodules"  
 /dev\_stage="effective root nodules harvested one month  
 post inoculation with Sinorhizobium meliloti"  
 /lab\_host="E. coli strain XL0R"  
 /note="Vector: Bluescript SK-; Site: 1: EcoRI; Site: 2:  
 XhoI; cDNA was prepared from polyA+ enriched RNA from  
 effective root nodules harvested one month post  
 inoculation with Sinorhizobium meliloti. The cDNA was  
 directionally ligated into the Uni-ZAP XR vector from  
 StrataGene and packaged using GigaPack III Gold packaging  
 extracts. Plasmids containing cDNA inserts were excised  
 from the recombinant lambda-ZAP phage using Ex-Assist  
 helper phage and propagated in XL0R cells."  
 BASE COUNT 186 a 134 c 144 g 181 t 1 others  
 Query Match 58.3%; Score 396.8; DB 9; Length 646;

Best Local Similarity 77.6%; Pred. No. 6e-110;  
 Matches 479; Conservative 0; Mismatches 138; Indels 0; Caps 0;  
 QY 64 ATGGGTGAGGCTGTTGGGTATGGGAATTTATACGCCAAGGATGAGCAGCAACGGTG 123  
 Db 2 ATGGGAGGGGCTTGTTGGTATGGAATTTGATAGCAAGGCTATGGAACCAACGCTCT 61  
 QY 124 GCGCTGAGCAGCTGCGCTATTTAACAAATGATTAAGTTGGTGGCTTGGTGAATGACT 183  
 Db 62 GCAGTAAGCAGCTGCTTTTACAAATGATTTGATTTGGGTCTTGGTACGAGATGAA 121  
 QY 184 TGTACAAAGACCTTAATATGTTGCTCCGGCACTATTAAGCTACCTGCCAACAATTT 243  
 Db 122 TGTACAGAGACCTTAATATGTTGCTCCGGCACTATTAAGCTACCTGCCAACAATTT 181  
 QY 244 TGGCCTCTCACTTGTCTCTCTTACAAACATGTTGATGTTGATGTTGATGTTGAT 303  
 Db 182 TGGCCTCTCACTTGTCTCTCTTACAAACATGTTGATGTTGATGTTGATGTTGAT 241  
 QY 304 CACTTCGACATGCTGAGCGCTGCTTCCCTCAATCGCTCAATACGAGCTGATGCTC 363  
 Db 242 CACTTTGATCTTGTGAGCGCTGCTTCCCTCAATCGCTCAATACGAGCTGATGCTC 301  
 QY 364 CCGCTCTCTTGTGAGCGCTGCTTCCCTCAATCGCTCAATACGAGCTGATGCTC 423  
 Db 302 CCTATTTCTCTGAGAGAGTACCTGTTTGAAGAAAGAGAGATCAATATCAATAT 361  
 QY 424 GGCACATCACTTATCACTGCTTTTATCAACAACGCTGCTGCGCAGCGAGCTCCAC 483  
 Db 362 GGCACATCACTTATCACTGCTTTTATCAACAACGCTGCTGCGCAGCGAGCTCCAC 421  
 QY 484 TCTGTGATGATTAAGGGGCTGCAAGCTGATGCGCAATCATGCTATGAAATTTGGGCGCA 543  
 Db 422 TTTGTGTCATCAAGGATCAAGCTGATGCGCAATCATGCTATGAAATTTGGGCGCA 481  
 QY 544 AACTGCAAGCAAGCAACTATCAATGCGCAAGGCTTCTTCAAGTCACTCTTACT 603  
 Db 482 AACTGCAAGCAAGCAACTATCAATGCGCAAGGCTTCTTCAAGTCACTCTTACT 541  
 QY 604 GATGCTGCACTCTCACTGCTTATATCTGCTTCTTCAATTTGGCAATTTGGCAACC 663  
 Db 542 GATGCTGCACTCTCACTGCTTATATCTGCTTCTTCAATTTGGCAATTTGGCAACC 601  
 QY 664 TATGAAGGCCCTCAATT 680  
 Db 602 TTTACAGGGGCTCAATT 618  
 RESULT 4  
 BE131139 815 bp mRNA linear EST 20-FEB-2001  
 LOCUS BE131139  
 DEFINITION L48-109073 Ice plant Lambda Uni-Zap XR expression library, 48 hours  
 NaCl treatment Mesembryanthemum crystallinum cdna clone l48-1090  
 5', mRNA sequence.  
 ACCESSION BE131139  
 VERSION BE131139.1 GI:8578502  
 KEYWORDS EST.  
 SOURCE Common ice plant.  
 ORGANISM Mesembryanthemum crystallinum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllidae; Caryophyllales; Alzaceae; Mesembryanthemum.  
 1 (bases 1 to 815)  
 REFERENCE  
 AUTHORS Cushman, J.C.  
 TITLES An expressed sequence tag database for the common ice plant.  
 JOURNAL Mesembryanthemum crystallinum  
 COMMENT Unpublished (1997)  
 Department of Biochemistry  
 University of Nevada  
 MS200, Reno, NV 89557-0014, USA  
 Tel: 775-784-1918  
 Fax: 775-784-1650



QY	361	GTCCCGGCTCCCTCCCTTCGTAGGAGTACCATGTATGAGAAAGGTGGAGTGGCTTTCAATC	420
Db	373	GTCCCTGTTATGTTCAGAAAGGTGTCACTGTGTGAAAGAAAGAGGCATCAGTATACACATG	432
QY	421	AATGGCCACTCATCTTCAACCTCGTTTTGATCACAACGTCGCGGCGCAGGCACGTC	480
Db	433	AATGACACTTTCGTACTTCAACATGTGGCGATTTAAAGCAAGCTGGGAGGTGACAGGAGATATA	492
QY	481	CACCTGTGTGCATTAAGAGGGGTCTGCACTGGATGGCATCCCATGCTCTAGAATTTGGGC	540
Db	493	ACGTAGTGTCCATCAAGGGTTCACGAAAGAGATGGTCACTATCTCCAGAAATTTGGGCG	552
QY	541	CAAAACCTGGCAACCAACTATCTCAATGSGCCAAAGCCTTTCCTTCAAGTCACTCTT	600
Db	553	CAAAACCTGGCAAGGAAATGCTTAACTTAAAGCAAAAGCCTCTCTTTAAATGTAAGTGC	612
QY	601	AGTGAAGTGCAGCTCTACATCTATATATCTCGTTCCTCCCAATGGCAATTTGGCA	660
Db	613	AGCGATGGCAGGACTATTAACAGCTTACAATGTATGCGCTGTGGCAATTTGGACAA	672
QY	661	ACCTATGAAGGCCCTTCATTT	680
Db	673	ACTTTTGAAGCAAGCAAGT	692

RESULT 6	BE055631	LOCUS	DEFINITION
BE055631	966 bp	mRNA	linear
GA_E00031J22f	Gossypium	arborescens	7-10 dpa fiber library Gossypium
arborescens CDNA clone GA_E00031J22f,			mRNA sequence.

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VERSION      BE055631.2  GI:13245739
KEYWORDS
SOURCE
Gossypium arboreum.
EST.

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ORGANISM  
Gossypium arboreum  
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;  
Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots;  
Rosidae: eurosids II: Malvales: Malvaceae: Gossypium.  
1 (bases 1 to 966)  
Wing, R.A., Fritsch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry

TITLE	An integrated analysis of the genetics, development, and evolution of the cotton fiber
JOURNAL	Unpublished (2000)
COMMENT	On Jun 8, 2000 this sequence version replaced gi:382688.

Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: [twing@clemson.edu](mailto:twing@clemson.edu)  
Seq primer: TAATACGACTCACAATAGCG  
High quality sequence start: 4  
High quality sequence stop: 945.

BASE COUNT	ORIGIN	SOURCE
266	a	1. : 966 /organism="Gossypium arboreum" /strain="AKA" /cultivar="8400" /db_xref="taxon:29729" /clone="GA_EA0031J22f" /clone_1lb="Gossypium arboreum 7-10 dpa fiber library" /tissue_type="Fibers isolated from bolls harvested 7-10 dpa" /lab_host="E. coli" /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
266	a	201 c
241	g	257 t
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Query Match      56.1%; Score 382; DB 9; Length 966;
Best Local Similarity 73.0%; Pred. No. 2.5e-105;
Matches 490; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

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Db	36	G	A	C	A	T	G	G	T	G	T	G	C	A	A	C	T	G	C	A	C	T	T	C	T	A	G	G	T	G	T	G	A	C	T	G	95	
QY	61	A	C	C	A	T	G	G	T	G	T	G	A	T	T	A	T	A	T	A	C	A	C	C	A	A	G	G	T	A	T	G	C	A	A	C	120	
Db	96	A	C	A	A	T	G	G	G	G	A	G	C	T	T	G	T	T	A	T	G	A	A	A	C	C	T	T	A	T	G	A	A	A	C	155		
QY	121	G	T	G	C	C	T	G	A	G	C	A	T	T	T	A	A	C	A	A	T	G	A	T	T	A	G	T	T	G	T	G	T	G	A	180		
Db	156	G	C	A	G	T	T	G	C	A	C	T	T	T	C	A	A	A	T	G	C	T	T	G	A	C	T	T	G	C	T	G	C	T	G	215		
QY	181	A	C	T	T	G	A	C	A	A	G	A	C	C	C	A	A	T	A	T	A	T	G	T	G	C	C	T	C	C	G	G	A	C	A	240		
Db	216	C	G	T	G	C	A	C	A	A	T	G	A	T	T	A	T	T	A	T	T	A	T	T	A	T	T	A	T	T	A	T	T	A	275			
QY	241	T	T	T	T	C	C	C	T	C	T	A	C	T	T	T	C	C	T	C	C	T	C	C	T	A	C	A	A	C	A	A	T	G	300			
Db	276	T	T	T	T	G	C	A	C	A	T	A	T	G	C	T	T	A	T	C	T	A	T	C	T	A	T	G	A	C	A	A	T	G	335			
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QY	361	G	T	C	C	C	C	G	T	C	T	T	C	T	T	G	T	A	G	G	T	A	C	A	T	G	A	A	A	G	A	A	G	T	A	420		
Db	396	G	T	C	C	T	T	A	T	T	C	A	A	G	G	T	G	T	A	C	A	T	G	A	A	A	G	A	A	G	A	A	G	T	A	455		
QY	421	A	A	T	G	C	A	C	T	A	T	C	A	A	C	T	G	T	T	T	G	A	T	C	A	A	A	C	T	G	T	G	C	A	480			
Db	456	A	A	T	G	C	A	T	T	C	T	A	C	T	T	A	A	C	A	T	G	C	G	T	T	G	A	A	A	C	T	G	T	G	515			
QY	481	C	A	C	T	G	T	G	T	C	A	T	A	A	G	G	G	T	C	G	A	A	C	T	G	A	A	C	T	G	A	A	C	A	540			
Db	516	A	C	G	T	A	G	T	C	A	A	G	G	T	C	C	A	A	G	A	T	G	C	A	T	C	A	T	A	T	G	C	A	575				
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Db	576	C	A	A	A	C	T	G	C	A	A	G	A	T	C	T	A	A	C	T	T	A	A	C	G	A	A	G	C	A	A	G	C	A	635			
QY	601	A	A	T	G	A	T	G	T	G	C	A	T	C	A	T	A	T	A	T	C	T	G	T	C	T	C	A	A	T	T	G	C	A	660			
Db	636	A																																				

RESULT 7	BE034856	775 bp	linear	EST 07-JUN-2000
LOCUS	BE034856			
DEFINITION	ML050C12 ML Mesembryanthemum crystallinum cDNA 5', mRNA sequence.			
ACCESSION	BE034856			

KEYWORDS	MEB-94-050.1, 01.0325005
EST.	
SOURCE	Common ice plant.
ORGANISM	Mesembryanthemum crystallinum
AUTHORS	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Caryophyllidae: Caryophyllales: Alzooceae, Mesembryanthemum: 1 (bases 1 to 775)
REFERENCE	Bohnert, H. J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferreira, H., Kawasaki, S., McCollough, A., Michalowski, C. B., Palacio, C., Scara, G., Wheeler, M. and Zepeda, G. R.
TITLE	Functional Genomics of Plant Stress Tolerance
JOURNAL	Unpublished (2000)
COMMENT	Contact: Michalowski, C. B.

ONAR, S. & J. C. HILLIS  
Bio Sciences West room 513, Tucson, AZ 85721, USA  
Tel: 520-621-7982  
Fax: 520-621-1697

Email: cbmew.arizona.edu  
An open reading frame exists.  
Location/Qualifiers

FEATURES  
source  
1..775  
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/clone\_lib="ML"  
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/note="6 weeks in 500mM NaCl"

BASE COUNT 188 a 207 c 181 g 198 t 1 others  
ORIGIN

Query Match 54.2%; Score 368.8; DB 9; Length 775;  
Best Local Similarity 75.5%; Pred. No. 2.3e-101;  
Matches 471; Conservative 0; Mismatches 152; Indels 1; Gaps 1;

Oy 7 GGTGGTCGACAGCGGCCACGCTTTTATGTCGTGATGACGATCTGCACCATG 66  
Db 144 GGTGGTCGACAGCGGCCACGCTTTTATGTCGTGATGACGATCTGCACCATG 203  
Oy 67 GGTGGTCGACAGCGGCCACGCTTTTATGTCGTGATGACGATCTGCACCATG 126  
Db 204 GGTGGTCGACAGCGGCCACGCTTTTATGTCGTGATGACGATCTGCACCATG 263  
Oy 127 GGTGGTCGACAGCGGCCACGCTTTTATGTCGTGATGACGATCTGCACCATG 186  
Db 264 TTAAGACAGCGGCCACGCTTTTATGTCGTGATGACGATCTGCACCATG 323  
Oy 187 ACAAGACAGCGGCCACGCTTTTATGTCGTGATGACGATCTGCACCATG 246  
Db 324 AACAGACAGCGGCCACGCTTTTATGTCGTGATGACGATCTGCACCATG 383  
Oy 247 CACCTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 306  
Db 384 CACCTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 443  
Oy 307 TTAAGACAGCGGCCACGCTTTTATGTCGTGATGACGATCTGCACCATG 366  
Db 444 TTAAGACAGCGGCCACGCTTTTATGTCGTGATGACGATCTGCACCATG 503  
Oy 367 GGTGGTCGACAGCGGCCACGCTTTTATGTCGTGATGACGATCTGCACCATG 426  
Db 504 AACAGACAGCGGCCACGCTTTTATGTCGTGATGACGATCTGCACCATG 563  
Oy 427 CACCTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 486  
Db 564 CACCTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 623  
Oy 487 GGTGGTCGACAGCGGCCACGCTTTTATGTCGTGATGACGATCTGCACCATG 546  
Db 624 GGTGGTCGACAGCGGCCACGCTTTTATGTCGTGATGACGATCTGCACCATG 683  
Oy 547 TTAAGACAGCGGCCACGCTTTTATGTCGTGATGACGATCTGCACCATG 605  
Db 684 TTAAGACAGCGGCCACGCTTTTATGTCGTGATGACGATCTGCACCATG 743  
Oy 606 TTAAGACAGCGGCCACGCTTTTATGTCGTGATGACGATCTGCACCATG 629  
Db 744 CGAGACAGCGGCCACGCTTTTATGTCGTGATGACGATCTGCACCATG 767

RESULT 8  
LOCUS B1309709 741 bp mRNA linear EST 20-JUL-2001  
DEFINITION EST531119 GP0D Medicago truncatula cDNA clone pGP0D-13L4 5' end,  
ACCESSION B1309709  
VERSION B1309709.1 GI:14984036  
KEYWORDS EST.  
SOURCE barrel medic.  
ORGANISM Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE  
AUTHORS 1 (bases 1 to 741)  
TITLE Grusak, M.A., Samac, D.A., Town, C.D., Van Aken, S., Utterback, T., Cho, J., and Fraser, C.M.  
JOURNAL ESTs from developing reproductive tissues of Medicago truncatula  
COMMENT Unpublished (2001)  
Contact: Michael A. Grusak  
USDA/ARS Children's Nutrition Research Center  
Baylor College of Medicine  
1100 Bates Street, Houston, TX 77030-2600, USA  
Tel: 713-798-7044  
Fax: 713-798-7078  
Email: mgrusak@bcm.tmc.edu  
B396564e

FEATURES  
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1..741  
/organism="Medicago truncatula"  
/cultivar="A17"  
/db\_xref="taxon:3880"  
/clone\_lib="pGP0D-13L4"  
/clone\_lib="GP0D"  
/issue\_type="immature pod walls"  
/dev\_stage="immature pods, ranging in age from 15 to 30 days after pollination"  
/note="Vector: pBluescript SK-; Site-1: EcoRI; Site-2: XhoI; Immature pods, ranging in age from 15 to 30 days after pollination, were collected from greenhouse-grown plants. At harvest, seeds were removed from pods and isolated pod walls were collected and immediately frozen in liquid nitrogen. Pod walls were pooled for mRNA extraction. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL0R cells."

BASE COUNT 206 a 157 c 163 g 215 t  
ORIGIN  
Query Match 54.0%; Score 367.8; DB 10; Length 741;  
Best Local Similarity 78.0%; Pred. No. 4.6e-101;  
Matches 455; Conservative 0; Mismatches 127; Indels 1; Gaps 1;  
Oy 2 ACTACGGTGGTCGACAGCGGCCACGCTTTTATGTCGTGATGACGATCTGCAC 61  
Db 159 ACGAGGTGGATGGGAAATGCTCATGCCACATTTATGTCGTGATGACGATCTGCAC 218  
Oy 62 CCATGGTGGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 121  
Db 219 CAAATGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 278  
Oy 122 TGGCGTGGAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 181  
Db 279 CTGACATAGTACTGCTCTTTCAACATGATGATGATGATGATGATGATGATG 338  
Oy 182 CTGTACAAAGCAGCCTTAATGTCCTTCCGGAAGCTATTAGGCTACCTCCACA 241  
Db 339 AATGTACAGTACCCCTTAATGTCCTTCCGGAAGCTATTAGGCTACCTCCACA 398  
Oy 242 TTTGGCTCTTACTTTGCTTCCCTAACACATGATGATGATGATGATGATGATG 301  
Db 399 TCTGCCCCCAAACTTGGAGAGCTAATACCAATGATGATGATGATGATGATGAT 458  
Oy 302 AACACTTGCAGATGGTGGAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 361  
Db 459 AGCAGCTTATCTTGTGTAGAGCTGCTTCTTCAATATGCTCAATACCAAGCTGA 518  
Oy 362 TCCCGTCTCTTGTGTAGAGCTGATGATGATGATGATGATGATGATGATGATG 421

[illegible]

D6		62	TTGAGCTGTGGAGCGTTCCTATGAATAATGAATTGTAACGACGACCAGAANTGGTGCAACCCA	121
OY		214	GGAACCTTTTAGGGTCACTGCCACCAACTTTTGGCCCTCCTAACTTTGGTCCCTAACAC	273
D6		122	GGAAGCATTTATAGTCACTGCCTAATTTTGGCCACCACTTTGGTGGCTAACAC	181
OY		274	AATGGTAGATGGTGCACACCCCTCTCTCCAAACACTTTCGACATGGCTGAGCCTGGCTTCTT	333
D6		182	AATGGTAGATGGTGCACACCCCTCTCTCCAAACACTTTCGACATGGCTGAGCCTGGCTTCTT	333
OY		334	CAAAATGCGTCATATCCGAGCTGTATCGTCCCCTCTCTTTGGTAGGGTACCATGTATG	393
D6		242	AAGATTCGCCCAATCAAAAGCTGGAAATGATCTTATTCCTTCAAGAAAGGATACCTGTATG	301
OY		394	AGAAAGGTGGAGTAGAGTTTACAAATCAATGAGCCACTCATTAACCTTCAACCTCGTTTTGATC	453
D6		302	AGAAAGGTGGAGTAGAGTTTACAAATCAATGAGCCACTCATTAACCTTCAACCTCGTTTTGATC	361
OY		454	ACAACAGTCGTGGTGGCGCACGAGCGTCCACTCTGTGTCGATTAAGGGGCTTCGACATGGA	513
D6		362	TCCAACTGGTGGTGGCGCGGTGACGTCCACTCTGTGTCGATTAAGGGGCTTCGACATGGA	421
OY		514	TGGCACTCATATGTCTAGAAATTTGGGGGCCAAAACGTGGCAAACCAACACTATCTCAATGGC	573
D6		422	TGGCAACCAATGTCAGAAACCTGGGGCCAAAACGTGGCAAATTAACCTTACCTCAAGGCG	481
OY		574	CAAGGCGTTTCCTCTTCAAGTCACTCTTATGATGATGGTGGCACTCTCACTGCTATTAATCTC	633
D6		482	CAGAGCCCTGCTCTTCAAGGTTACCGCTGTGACGACGAGACGAGCGATGACGACACACATTT	541
OY		634	GTTCCCTTCAATTTGGCAATTTGGCCAAACCTATGCAAGGCCCTCAATTC	681
D6		542	GTTCCCTTCAATTTGGCAATTTGGCCAGACATTTGGGCTGGCCAAATTC	589
RESULT 10				
LOCUS	AW776306			
DEFINITION	ESTJ35J517 DStL Medicago truncatula cDNA clone pDStL-7M2, mRNA sequence.	668 bp	mRNA	linear EST 07-SEP-2000
ACCESSION	AW776306			
VERSION	AW776306.1 GI:7766119			
KEYWORDS	EST.			
SOURCE	bareil medic.			
ORGANISM	Medicago truncatula			
REFERENCE	1 (bases 1 to 668)			
AUTHORS	Fedorova,M., Plesion,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Peng,H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.			
TITLE	ESTs from leaves of Medicago truncatula after inoculation with Colletotrichum trifolii			
JOURNAL COMMENT	Unpublished (2000) Contact: Deborah A. Samac Department of Plant Pathology University of Minnesota 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA Tel: 612 625 1243 Fax: 651 649 5058 Email: debbysepuc@t.crl.umn.edu Minnesota sequence name:M259633e TIGR sequence name:MTFAH73TK More information is available at: <a href="http://chryslie.tamu.edu/medicago">http://chryslie.tamu.edu/medicago</a> Seq primer: Skmod (CPA gaa gta gat CC). Location/Qualifiers 1..668 /organism="Medicago truncatula" /cultivar="genotype A17" /db_xref="taxon:3880"			
FEATURES	Source			



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/clone="pDSIL-7M2"
/tissue_type="leaves infected with Colletotrichum
trifolii"
/dev_stage="cotyledons and primary leaves harvested 5 and
8 days after inoculation with Colletotrichum trifolii"
/lab_host="E. coli strain XLOLR"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
cotyledons and primary leaves harvested 5 and 8 days after
inoculation with Colletotrichum trifolii. The cDNA was
directionally ligated into the Uni-ZAP XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-ZAP phage using Ex-Assist
helper phage and propagated in XLOLR cells. Note: EST may
be of fungal origin."
BASE COUNT      181 a      118 c      156 g      213 t
ORIGIN

```

```

Query Match      52.8%; Score 359.4; DB 9; Length 668;
Best Local Similarity 78.1%; Pred. No. 1.6e-98;
Matches 432; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

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QY 1 GACTAGCGTGGCTGGGAGAGCGGCGACCTTTTATGTCGGTACGCATCTGAC 60
DB 116 GATTATGTTGGTGGAGAGTGGTCTTCTTCTATGTCGTCGTCGTCGTCGTC 175
QY 61 ACCATGGGTGAGAGCTGGTGGTATGGGAATTTATACAGCGGATGAGCGACAG 120
DB 176 ACAATGGGTGAGAGCTGGTGGTATGGGAATTTATACAGCGGATGAGCGACAG 235
QY 121 GTGGCGCTGAGCAGCTGGCTATTTAACAATGATTAAGTTGGTGGCTTCTTCA 180
DB 236 GCGAGCTAGGAGCTGCTTGTTCACAACAAATGTTTAAAGCTGGATGATGAATG 295
QY 181 ACTTGTACAAAGCAGCTTAAATGTCCTCCGGGAACATTAAGGTCACCTCCAC 240
DB 296 AGATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 355
QY 241 TTTTGGCTGCTTAACTTGTCTCTCCCTTAAACAATGATGATGATGATGATGAT 300
DB 356 TTTTGGCTGCTTAACTTGTCTCTCCCTTAAACAATGATGATGATGATGATGAT 415
QY 301 CAACACTTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 416 CAACACTTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 475
QY 361 GTCCCGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 420
DB 476 GTGCGCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 535
QY 421 AATGGCAGCTACTTCACTCTGTTTGTATCAACAAGTGGTGGCGAGCGAGCTC 480
DB 536 AATGGCAGCTACTTCACTCTGTTTGTATCAACAAGTGGTGGCGAGCGAGCTC 595
QY 481 CACTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 596 CATTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 655
QY 541 CAAAACCTGGCAAA 553
DB 656 CAAAATTTGGCAAA 668

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RESULT 11
LOCUS      BE584282
DEFINITION 7-3E-HA Psojaeha Glycine max/Phytophthora sojae mixed EST library
ACCESSION BE584282
VERSION    BE584282.1 GI:9835231
KEYWORDS   EST.

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SOURCE      Glycine max/Phytophthora sojae mixed EST library.
ORGANISM    Glycine max/Phytophthora sojae mixed EST library
REFERENCE    1 (bases 1 to 654)
AUTHORS      Qutob,D., Hraber,P.T., Sobral,B.W.S. and Gijzen,M.
TITLE        Comparative analysis of expressed sequences in Phytophthora sojae
JOURNAL      Plant Physiol. 123 (1), 243-254 (2000)
MEDLINE      20267956
COMMENT      Contact: Gijzen M
              Agriculture and Agri-Food Canada
              1391 Sandford Street, London, Ontario, Canada N5V 4R3
              Tel: 519 457 1470
              Fax: 519 457 3997
              Email: gijzenm@em.agr.ca
              Transcript obtained from mixed plant-pathogen interaction culture.

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FEATURES
    source
        1..654
            /organism="Glycine max/Phytophthora sojae mixed EST
            library"
            /strain="Phytophthora sojae race 2 strain P6497"
            /cultivar="Glycine max cultivar Harsoy"
            /db_xref="taxon:135715"
            /clone_id="Psojaeha"
            /tissue_type="Plant hypocotyls infected with Phytophthora
            sojae"
            /dev_stage="8 d old etiolated hypocotyls 48 h
            post-inoculation with Phytophthora sojae zoospores"
            /lab_host="E. coli strain XLOLR"
            /note="Vector: pBK-CMV; Site 1: EcoRI; Site 2: XhoI; This
            cDNA library was constructed from polyA+ enriched mRNA
            from etiolated hypocotyls 48 h post-inoculation with
            Phytophthora sojae zoospores. Complementary DNA was
            synthesized from mRNA using an XhoI-poly(dT)
            linker-primer. EcoRI adapters were ligated to the
            blunt-ended cDNA fragments and the products were digested
            with XhoI for directional cloning into lambda ZAP Express
            vector. This lambda library was amplified once using E.
            coli host strain XL1 Blue MRF+. Inserts were then
            subcloned by mass excision using ExAssist helper phage
            for conversion into phagemid vector pBK-CMV in E. coli
            host strain XLOLR. Sequenced using T3 primer: 5' ATT AAC
            CCT CAC TAA AGG GA 3'."

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```

BASE COUNT      172 a      150 c      148 g      184 t
ORIGIN

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Query Match      52.7%; Score 358.6; DB 10; Length 654;
Best Local Similarity 76.6%; Pred. No. 2.7e-98;
Matches 439; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

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QY 109 GGCAGCAACAGGTGGCGCTGAGCAGCTGCGCTATTAAACAATGATTAAGTTGGTGT 168
DB 1 GGAACCAACACTGCAGCAGCAGCAGCTGCTATTAAACAATGATTAAGTTGGTGT 60
QY 169 TGTCTGAATGAGTCTTACAAAGACCTTAATGTCCTTCCGGAGCTATTAGGCTC 228
DB 61 TGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 229 ACTGCGACCAACTTTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 288
DB 121 ACTGCGACCAAACTTCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 180
QY 289 AACCTCTCTTCAACACTTGCAGATGCTGAGCGCTGCTTCAAAATGCTCAATAC 348
DB 181 AACCTCTCTTCAACACTTGCAGATGCTGAGCGCTGCTTCAAAATGCTCAATAC 240
QY 349 CGAGCTGTATGCTCCCGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 408
DB 241 AAGCTGTGATTTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 300
QY 409 AGTTTAAATCAATGAGCAGCTACTTCAACCTGTTTGTATCAACAACGTCGGTGGC 468
DB 301 AGTTTAAATCAATGAGCAGCTACTTCAACCTGTTTGTATCAACAACGTCGGTGGC 360

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Email: <http://www.genome.clemson.edu/orders/index.html>  
This clone is available through the Clemson University Genomics Institute

FEATURES Seq primer: T3.  
Location/Qualifiers  
1. 710  
/organism="Lycopersicon esculentum"  
/cultivar="T496"  
/clone="CTOC18N14"  
/clone\_1lb="tomato flower, 8 mm to preanthesis buds"  
/tissue\_type="flower"  
/dev\_stage="buds 8mm to preanthesis"  
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Cornell University; sequencing: The Institute for Genomic Research; Flower buds and flowers were taken from greenhouse plants (4-8 wks old, T496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."

BASE COUNT 187 a 143 c 147 g 233 t  
ORIGIN

Query Match 52.3%; Score 356; DB 10; Length 710;  
Best Local Similarity 75.2%; Pred. No. 1.8e-97;  
Matches 457; Conservative 0; Mismatches 150; Indels 1; Gaps 1;

QY 1 GACTACGCTGGCGACAGCGCCGACGACCTTTTATGGTGGTGGACATCTGGC 60  
DB 100 GATTATGGAGATGGCAACTCTCATGCGACTTCTATGAGGGGATGCTCTGGC 159  
QY 61 ACCATGGGTGAGACTTGTGGTATGGAAATTTACAGCAAGGGTATGGCAGACAG 120  
DB 160 ACAATGGGGGTGCTTGATGATGAAATTTGTATGCAAGGGTATGGAACACT 219  
QY 121 GTGGCGCTGACACTGCGCTATTTAACATGATTAAGTTGGTGGCTTGCATG 180  
DB 220 GCAGCACTAAGACACACTATTCAACATGTTTAACTTGGTGGCTTGTATAGCTC 279  
QY 181 ACTTTACAAAGACACCTAATGATGCTTCCGGAATATTAGGCTACCTCCACCA 240  
DB 280 ACTTGCAACATGACACTCATATGATGCTCCAAAGGACATATTCTGCTCACTA 339  
QY 241 TTTTGGCTCTTAACTTTGCTCTCCCTAACACATATGGTGGTGGCAACCTCTC 300  
DB 340 TTTTGTCTTCCGAAACCGCTCTACCTAACATTAATGTTGGTGGCAATCTCTC 399  
QY 301 CAACACTTGGACATGGCTGAGCTCTCTCAATGCTCAATATCCAGAGCTGTATC 360  
DB 400 CAACATTTGATTTAGCACACACTGCTTCTTGCAATATGCTAATATACAAAGCG 459  
QY 361 GTCCCGCTCTCTTTGTAGGATCATGATGAGAAAGGTGGAGTGTACATATC 420  
DB 460 GTCCCTGTATCTTTGGAAGGGTGGCTGTATGAGAAAGGAGAAATAGGTTAC 519  
QY 421 AATGGCACTCATCTTCAACCTCGTTTGTATGACAAAGCTGGCGAGGCGACGTC 480  
DB 520 AATGGACATCATTTTCACTTGTGTTTATGACAAAGTGTGAAGTGTGCTATAT 579  
QY 481 CACTCTGTGCTAATAAGGGCTCTCGAACTGATGGCAATCATCTGTAGAAATGG 540  
DB 580 TCATCACTTTCATTA- GGGCTTAATATCTGATGGCAACATATGCAAGAAAT 638  
QY 541 CAAAATGGCAAAACAACTATCTCAATGGCCAGGCTTCTTCAAGTCACTCTT 600  
DB 639 CAAAATGGCAAAACAACTTCAATCTAATGATGCTCAAGTCTTCAATGTCAC 698  
QY 601 AGTATGG 608  
DB 699 AGTATGG 706

RESULT 14  
AWS84547 695 bp mRNA linear EST 07-SEP-2000  
LOCUS N210609e MHAM Medicago truncatula/Glommus versiforme mixed EST  
DEFINITION library cdna clone MHAM-ZP17, mRNA sequence.

ACCESSION AWS84547  
VERSION AWS84547.1 GI:7261601  
KEYWORDS EST.  
SOURCE Medicago truncatula/Glommus versiforme mixed EST library.  
ORGANISM Medicago truncatula/Glommus versiforme mixed EST library.  
REFERENCE Eukaryota: mixed EST libraries.  
1 (bases 1 to 695)  
AUTHORS Harrison M.J., Liu J., Peng H., Gonzales M., Ellis L., Town C.D., Bowman C.L., Craven M.B., Hansen T.S., Holt I.E. and Fraser C.M.  
ESTs from roots of Medicago truncatula after colonization with  
TITLE Glommus versiforme  
JOURNAL Unpublished (2000)  
COMMENT Contact: Harrison M.J.  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73401  
Tel: 580-223-5810  
Fax: 580-221-7380  
Email: mjharrison@noble.org  
Other name: MHAM-2c-C09; Date: 3/14/00; updated to the Database of  
Expressed Sequence Tags (dbEST) on 04/27/00; More information is  
available at <http://chrysis.tamu.edu/medicago/>.  
Seq primer: T3.  
Location/Qualifiers  
1. 695  
/organism="Medicago truncatula/Glommus versiforme mixed EST  
library"  
/cultivar="Medicago truncatula genotype A17"  
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/clone="MHAM-2P17"  
/clone\_1lb="MHAM"  
/tissue\_type="roots colonized with Glommus versiforme"  
/dev\_stage="roots harvested at 10, 17, 22, 31 and 38 days  
post-inoculation with Glommus versiforme. The library was  
made from a mixture of RNA from each of these stages."  
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; CDNA was prepared from polyA+ enriched RNA from  
roots harvested at 10, 17, 22, 31 and 38 days  
post-inoculation with Glommus versiforme. The CDNA was  
directionally ligated into the UniZap Xk vector from  
stratagene and packaged using GigaPack III Gold packaging  
extracts. Plasmids containing cDNA inserts were excised  
from the recombinant lambda-Zap phage using Ex-assist  
helper phage and propagated in XLOLR cells."

BASE COUNT 185 a 150 c 156 g 204 t  
ORIGIN

Query Match 52.0%; Score 353.8; DB 9; Length 695;  
Best Local Similarity 78.4%; Pred. No. 8.3e-97;  
Matches 424; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

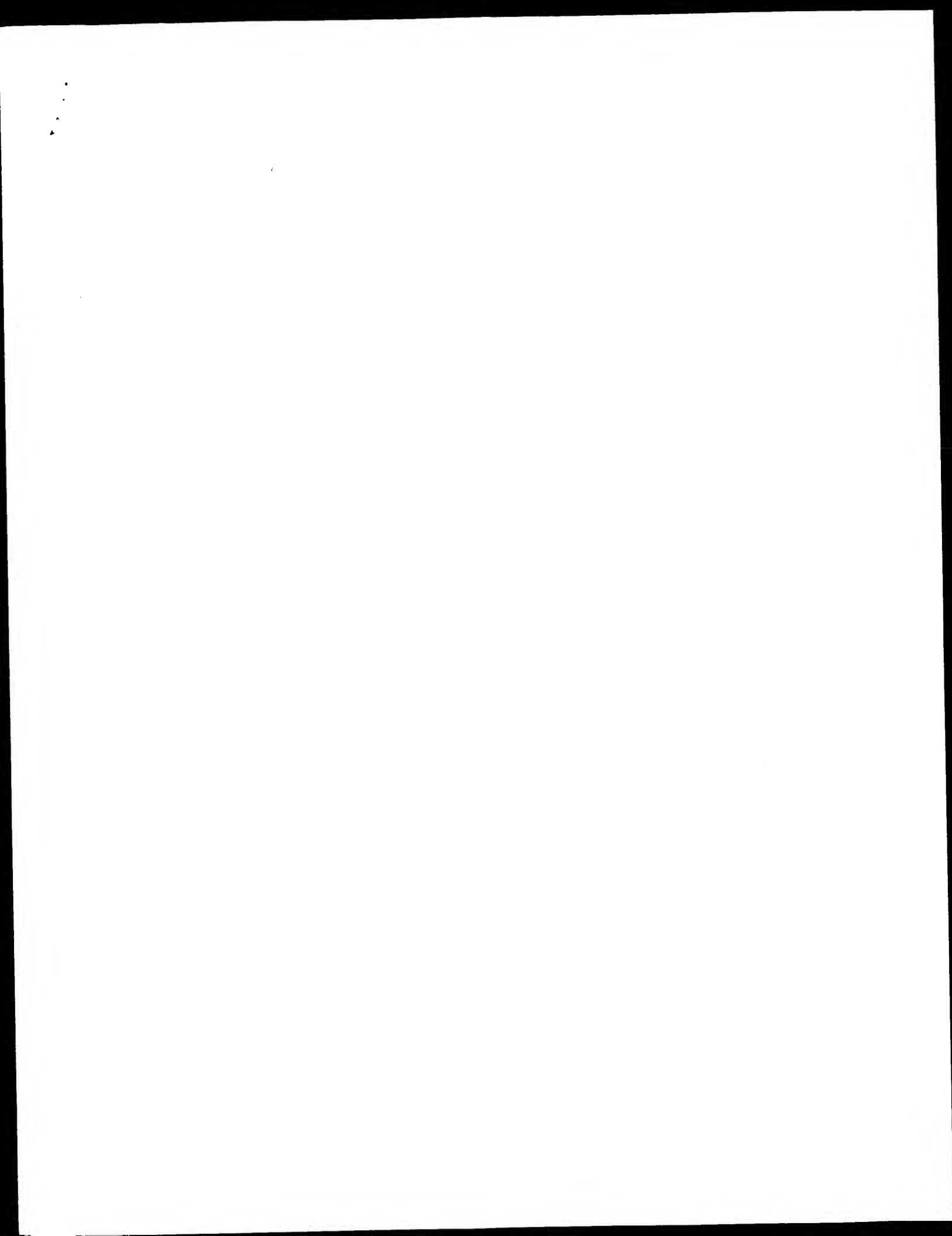
QY 7 GTGTGCTGGCAGAGCGCCGACGACCTTTTATGTTGTTGTTGACGATCTGGACCATG 66  
DB 155 GTGTGATGGGAATAAGCCCATTTTATGTTGATGAGAGATGATGCTACGAGCAATG 214  
QY 67 GTGTGAGCTTGTGGTATGGAATTTATACAGCCAAAGGATGTTGGCAGCAACGTTGGC 126  
DB 215 GGAGGGCTTGTGTTATGAGAAATTTGTAAGCCAAAGCTATGAAACCAACAGCTGCA 274  
QY 127 CTGAGACTGCGCTATTAAATGATTAAGTTGTGCTTGTCTGGAATGACTTGT 186  
DB 275 CTAGACACTGCTCTTTCAACAATGATGATGTTGCTGTACAGATGAAATGT 334  
QY 187 ACAAGGACCTTAATGTTGCTTCCGGAGCTATTAAGGTCACGTCAGCAACATTTTGGC 246  
DB 335 AACAGTGAACCTTAATGTTGCTTCCGTGTACATATTGTTACTACAACTTCTGCG 394  
QY 247 CCTCTAATCTTGTCTCTCTTAACAACATGATGATGTTGCAACCTCTCTCCACAC 306  
DB 395 CCCCACAACTTTGACAGAGCTTAATACCAATGTTGATGTTGCAACCTCTCTTACAGAC 454  
QY 307 TTGACATGCTGAGGCTCTCTCTCAATGCTCAATACGCAAGTGTGTTGCTCCCG 366

Query Match	52.0%;	Score 353.8;	DB 9;	Length 702;
Best Local Similarity	76.6%;	Pred. NO. 8.3e-97;		
Matches 433;	Conservative	0;	Mismatches 122;	Indels 0;
			Gaps	0;

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11		

Search completed: October 14, 2002, 00:08:00  
Job time : 1952 secs



121 GTGGCGCTGAGCAGCTGCGCTATTACCAATGCG

Db 121 GTGGCGCTGAGCACTGGCGCTATTAAACATGATTAAGTTGTGTGCTGCTTCAATG 180  
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QY 301 CAACACTTGCAGATGCTGAGCTGAGCTCTTCCCTTCAATGCGTCAATACGAGCTGTATC 360  
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Db 481 CACTCTGTGTCATGATGAGGGGTCTGCACTGATGCGAATTCATGCTAGAAATTTGGGCG 540  
QY 541 CAANAAGTGGCAAGCAACACTATCTCATGAGCGCAAGGCTTCCCTTCAAGTCACTCTT 600  
Db 541 CAANAAGTGGCAAGCAACACTATCTCATGAGCGCAAGGCTTCCCTTCAAGTCACTCTT 600  
QY 601 AGTATGTCGACACTGCTACTGCTATATATCTGTTCTTCCAAATTTGGCAATTTGGCCAA 660  
Db 601 AGTATGTCGACACTGCTACTGCTATATATCTGTTCTTCCAAATTTGGCAATTTGGCCAA 660  
QY 661 ACCATGAGAGGCCCTCAATTC 681  
Db 661 ACCATGAGAGGCCCTCAATTC 681

## RESULT 2

US-09-092-160-1

; Sequence 1, Application US/09092160C  
; Patent No. 6235466  
; GENERAL INFORMATION:  
; APPLICANT: Cosgrove, Daniel J  
; APPLICANT: McQueen-Mason, Simon  
; APPLICANT: Guillinan, Mark J  
; APPLICANT: Shepherd, Tatyana  
; APPLICANT: Shi, Jun  
; TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS  
; FILE REFERENCE: 1194/1C1140S3  
; CURRENT APPLICATION NUMBER: US/09/092,160C  
; EARLIER FILING DATE: 1998-06-05  
; EARLIER APPLICATION NUMBER: 08/440,517  
; EARLIER FILING DATE: 1995-05-12  
; EARLIER APPLICATION NUMBER: 08/242,090  
; EARLIER FILING DATE: 1994-05-12  
; EARLIER APPLICATION NUMBER: 08/060,944  
; EARLIER FILING DATE: 1993-05-12  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 681  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: cDNA cucumber  
; OTHER INFORMATION: expansin  
US-09-092-160-1

Query Match 100.0%; Score 681; DB 4; Length 681;  
Best local Similarity 100.0%; Pred. No. 1.3e+28;  
Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTAGGGTGGCTGGAGAGAGCGGCCACGACCTTTATGCTGTGTGTACCATCTGGC 60  
Db 1 GACTAGGGTGGCTGGAGAGAGCGGCCACGACCTTTATGCTGTGTGTACCATCTGGC 60  
QY 61 ACCATGGGTGAGCTGTGTGATGAGATTTATACAGCAAGGGTATGAGCGACGAACAG 120  
Db 61 ACCATGGGTGAGCTGTGTGATGAGATTTATACAGCAAGGGTATGAGCGACGAACAG 120  
QY 121 GTGGCGCTGAGCACTGCGCTATTAAACAATGATTAAGTTGTGTGCTTCTTCAATG 180  
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QY 361 GTCCCGCTCTCTTGTGATGAGGTACATGATGAGAAAGGTGAGTGTATACATC 420  
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Db 481 CACTCTGTGTCATGATGAGGGGTCTGCACTGATGCGAATTCATGCTAGAAATTTGGGCG 540  
QY 541 CAANAAGTGGCAAGCAACACTATCTCATGAGCGCAAGGCTTCCCTTCAAGTCACTCTT 600  
Db 541 CAANAAGTGGCAAGCAACACTATCTCATGAGCGCAAGGCTTCCCTTCAAGTCACTCTT 600  
QY 601 AGTATGTCGACACTGCTACTGCTATATATCTGTTCTTCCAAATTTGGCAATTTGGCCAA 660  
Db 601 AGTATGTCGACACTGCTACTGCTATATATCTGTTCTTCCAAATTTGGCAATTTGGCCAA 660  
QY 661 ACCATGAGAGGCCCTCAATTC 681  
Db 661 ACCATGAGAGGCCCTCAATTC 681

## RESULT 3

US-08-845-539-5

; Sequence 5, Application US/08845539  
; Patent No. 5929303  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, Alan B.  
; APPLICANT: Rose, Jocelyn K.C.  
; TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation  
; TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

```

: APPLICATION NUMBER: US/08/845.539
: FILING DATE: 25-APR-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
:   NAME: Bastian, Kevin L.
:   REGISTRATION NUMBER: 34,774
:   REFERENCE/DOCKET NUMBER: 023070-078200US
: TELECOMMUNICATION INFORMATION:
:   TELEPHONE: (415) 576-0200
:   TELEFAX: (415) 576-0300
:   INFORMATION FOR SEQ ID NO: 5:
:     SEQUENCE CHARACTERISTICS:
:       LENGTH: 537 base pairs
:       TYPE: nucleic acid
:       STRANDEDNESS: single
:       TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
:   NAME/KEY: CDS
:   LOCATION: 1..537
:   OTHER INFORMATION: /product= "melon CmeX1"
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: Query Match          40.6%; Score 276.4; DB 2; Length 537;
: Best Local Similarity 71.4%; Pred. No. 5.9e-87;
: Matches 380; Conservative 0; Mismatches 146; Indels 6; Gaps 1;
:
: QY 26 AGCCACCTTTTATGTTGCTGCTGACCGCATCTGGCACCATGGTGGAGCTTTGGGTATG 85
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: DB 5 ACCCCAGCTTTTATGAGCAGCGATGCTTCGGAACCATGGTGGTGGTCTTTGGGTATG 64
:
: QY 86 GGAATTTATACAGCCAGGATGAGCAGACACGCTGGCGGTGAGCACTGGCGATTATTA 145
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: DB 65 GCATCTCTACAGCCAGGCTATGCGCTACACACAGCTCTCTTACTGCTTTCTTTCA 124
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: QY 146 ACAATGATTAAGTTGCTGCTGCTTGGTGAATGACTTGTACAAACGACCCCTAAATGCT 205
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: DB 125 ACATGGCCCTACAGCTGTGGTCTTGTGAATCAAGTGTGCTAATGACCTCGATGCT 184
:
: QY 206 GCCTTCGGGGA-----CTATTAGGCTCAGTCCGACCAACTTTTCCCTCTACTTTG 259
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: DB 185 GCCATCTGTGATGCGCTTGTATCTTACCATTCACCAATTTTGTCCCTTAACCTTTG 244
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: QY 260 CTCCTCCCTACAAACATGGATGGATGGGACACCTCTCCCAACACTTGGCATGGCTG 319
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: DB 245 CTCCTCTAATGACAAATGGCGGTTGGTGTACCTTCTGCACTCAATTCGACCTGCTA 304
:
: QY 320 AGCCTGCTCTCTTCAATTCGCTCAATACCGAGCTGATCTGCCCTCTCTCTTTCTGA 379
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: DB 305 TGCCTATGTTCTCAAGATGCTGATGACCGCGCTGGAATCGGACCTGTCTTACCGCC 364
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: QY 380 GGGTACCATGTATGAGAAAGGTGAGTGGAGTGTACATCAATGGCCACTCTACTTCA 439
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: DB 365 GGGTTCATGTAGCAACAAGAGGAGATCAGTTTACAACTCAAGGTTTCCGTTACTTGA 424
:
: QY 440 ACCGCTGTTGATCACAACAGTGGTGGCGCAGGACGCTCACTGTGTCTGATTAAGG 499
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: DB 425 ATTTGGTGTATATCACCACAGCTGCGGGGTGCAAGGATATCTGAGAGGTAAAG 484
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: QY 500 GGTCTCGAAGTGGATGGCAATCCATGTCTAGAAATTTGGGGCAAAACTGGCA 551
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: DB 485 GATCAACACCGGTTGATGAGCATGATGCTAATTTGGGGCCAAACTGGCA 536
:
: RESULT 4
: US-09-362-642-5
: Sequence 5, Application US/09362642
: Patent No. 6350935
: GENERAL INFORMATION:
:   APPLICANT: Bennett, Alan B.
:   APPLICANT: Rose, Jocelyn K.C.
:   APPLICANT: The Regents of the University of California
:   TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes

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: TITLE OF INVENTION: to Control Fruit Texture and Softening
: FILE REFERENCE: 023070-078210US
: CURRENT APPLICATION NUMBER: US/09/362.642
: CURRENT FILING DATE: 1999-07-27
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: Patentln Ver. 2.1
: SEQ ID NO 5
: LENGTH: 537
: TYPE: DNA
: ORGANISM: Cucumis melo
: FEATURE:
:   NAME/KEY: CDS
:   LOCATION: (1)..(537)
:   OTHER INFORMATION: melon expansin (CmeX1) partial cDNA clone
:
: US-09-362-642-5
:
: Query Match          40.6%; Score 276.4; DB 4; Length 537;
: Best Local Similarity 71.4%; Pred. No. 5.9e-87;
: Matches 380; Conservative 0; Mismatches 146; Indels 6; Gaps 1;
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: QY 26 AGCCACCTTTTATGTTGCTGCTGACCGCATCTGGCACCATGGTGGAGCTTTGGGTATG 85
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: DB 5 ACCCCAGCTTTTATGAGCAGCGATGCTTCGGAACCATGGTGGTGGTCTTTGGGTATG 64
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: QY 86 GGAATTTATACAGCCAGGATGAGCAGACACGCTGGCGCTGAGCACTGGCGATTATTA 145
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: DB 65 GCATCTCTACAGCCAGGCTATGCGCTACACACAGCTCTCTTACTGCTTTCTTTCA 124
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: QY 146 ACAATGATTAAGTTGCTGCTGCTTGGTGAATGACTTGTACAAACGACCCCTAAATGCT 205
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: DB 125 ACATGGCCCTACAGCTGTGGTCTTGTGAATCAAGTGTGCTAATGACCTCGATGCT 184
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: QY 206 GCCTTCGGGGA-----CTATTAGGCTCAGTCCGACCAACTTTTCCCTCTACTTTG 259
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: DB 185 GCCATCTGTGATGCGCTTGTATCTTACCATTCACCAATTTTGTCCCTTAACCTTTG 244
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: QY 260 CTCCTCCCTACAAACATGGATGGATGGGACACCTCTCCCAACACTTGGCATGGCTG 319
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: DB 245 CTCCTCTAATGACAAATGGCGGTTGGTGTACCTTCTGCACTCAATTCGACCTGCTA 304
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: QY 320 AGCCTGCTCTCTTCAATTCGCTCAATACCGAGCTGATCTGCCCTCTCTCTTTCTGA 379
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: DB 305 TGCCTATGTTCTCAAGATGCTGATGACCGCGCTGGAATCGGACCTGTCTTACCGCC 364
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: QY 380 GGGTACCATGTATGAGAAAGGTGAGTGGAGTGTACATCAATGGCCACTCTACTTCA 439
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: DB 365 GGGTTCATGTAGCAACAAGAGGAGATCAGTTTACAACTCAAGGTTTCCGTTACTTCA 424
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: QY 440 ACCGCTGTTGATCACAACAGTGGTGGCGCAGGACGCTCACTGTGTCTGATTAAGG 499
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: DB 425 ATTTGGTGTATATCACCACAGCTGCGGGGTGCAAGGATATCTGAGAGGTAAAG 484
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: QY 500 GGTCTCGAAGTGGATGGCAATCCATGTCTAGAAATTTGGGGCAAAACTGGCA 551
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: DB 485 GATCAACACCGGTTGATGAGCATGATGCTAATTTGGGGCCAAACTGGCA 536
:
: RESULT 5
: US-07-885-970A-6
: Sequence 6, Application US/07885970A
: Patent No. 5495070
: GENERAL INFORMATION:
:   APPLICANT: John, Maliyakal E.
:   APPLICANT: John, Maliyakal E.
:   TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
:   NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
:   ADDRESS: Nicholas J. Seay, Quarles & Brady
:   STREET: P.O. Box 2113, First Wisconsin Plaza
:   CITY: Madison
:   STATE: Wisconsin
:   COUNTRY: USA
:   ZIP: 53701
: COMPUTER READABLE FORM:

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Query Match	38.1%	Score 259.4	DB 1	Length 727
Best Local Similarity	72.7%	Pred. No. 6.4e-81		
Matches 335	Conservative 0	Mismatches 126	Indels 0	Gaps 0
QY 220	ATTAGGCTACTGCCACCACTTTTGGCTCTCTAATCTTGCTCTCCCTAACCAACAATGTG	279		
Db 1	ATAACGGTGCACGCCACCAACTTTTGTCCACTACCTATGCTTTATCTAGTGAACATGGC	60		
QY 280	GGATGGGCAACCCCTCCTCCCAACACTTCGACATGGGTGAGCCTGCCCTTCCTCAATTC	339		
Db 61	GGGGTGGGCATCTCCCGACGAGAACACTTTGATTTGGCCGGAACGGCATCTTCGCGGATA	120		
QY 340	GCTCAATACGAGCTGTATGCTGCCCTGCTCCCTGCTTCGTAGGAGACCATGATGAAGAA	399		
Db 121	GCAGAAATATGAGACTGGATCTGCTCCCTGTATGTTCAGAAAGGCTGTATGTGTGAAGAA	180		
QY 400	GGTGGAGTAGGTTTACAATCAATGGCCACTCATACTTCAACTCTGTTTGTATCACAAC	459		
Db 181	GGAGGCACTCAGGTACACCATGAAATGGAATCTTGATCTTCAACATGAGTTGATAGCAAC	240		
QY 460	GTCGGTGGGCGAGCGCAGCTCACCTCTGTGTGCATAAAGGGGTCTCCAACTGGATGCCAA	519		
Db 241	GTCGGAGGGGCGAGGGGATTAACGTCACTGTGCATCAAGGGTCTCCAAACAGGATGGATA	300		
QY 520	TCCATCTTCAAAATTTGGGGCCAAACATGGGCAAGCAACACTTCTTCATTTGGCCAGAGG	579		
Db 301	CCATATGCCAGAAATTTGGGGCCAAACATGGGCAAGCAACACTTCTTCATTTGGCCAGAGG	360		
QY 580	CTTTCCTTCAAGTACTCTTATGATGATGGTGCACCTCTCACCTGCCATTAATCTCGTTCT	639		
Db 361	CTCTCTTTTAAAGTACTCCAGCATGGCAGGACTATACAGCGCTTCATTTGATGGCT	420		
QY 640	TCCAATTGGCAATTGGCCAAACCATATGAAGCCCTCAATT	680		

[illegible]

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Db 121 GCAGATATCGAGCTGGATGTCCTCTGTATGTTTCAAGAGGTCATGTCAGAAA 180
Oy 400 GGTGAGTGAAGTTTACAAATGATGGCAGCATCTTCAACCTCTTTGATCACAAC 459
Db 181 GGAGGCATCAGGTACACCATGATGAGCAATTCGACTTCAACATGAGGTGATTAACGAC 240
Oy 460 GTGCGTGGCCGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 519
Db 241 GTGGAGAGGGGAGGAGATATACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Oy 520 TCCATGCTGATGAATTTGGGCGCAAACTGCGCAAGCAACTATCTCAATGGCCAAAGC 579
Db 301 CCAATGTCAGAAATTTGGGCGCAAACTGCGCAAGCAACTATCTCAATGGCCAAAGC 360
Oy 580 CTTTCCTTTCAAGTCACTCTTGAAGTGTGCGCACTGCTGCTGCTGCTGCTGCTGCTGCT 639
Db 361 CTCTCTTTTAAAGTACATGCGCAGGATGCGCAGGATGCGCAGGATGCGCAGGATGCGCT 420
Oy 640 TCCAAATGGCAATTTGGCCAAACCTATGAAGGCCCTCAATT 680
Db 421 GCTGCTTGGCAATTCGCAAACTTTTGAAGGAGGCCAGTT 461

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## RESULT 7

US-08-530-797-5

Sequence 5, Application US/08530797

Patent No. 5597718

GENERAL INFORMATION:

APPLICANT: John, Mallyakal E.

APPLICANT: Umbeck, Paul F.

TITLE OF INVENTION: GENETICALLY ENGINEERED COTTON PLANTS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESS: Quarles and Brady

STREET: P.O. BOX 2113

CITY: MADISON

STATE: WISCONSIN

COUNTRY: U.S.A.

ZIP: 53701

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette - 3.50 inch, 800Kb storage

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh

SOFTWARE: Microsoft Word 4.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/530,797

FILING DATE: 20-SEP-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/617,239

FILING DATE: 21-NOV-90

APPLICATION NUMBER: US 07/253,243

FILING DATE: 04-OCT-88

ATTORNEY/AGENT INFORMATION:

NAME: Nicholas J. Seay

REGISTRATION NUMBER: 27,386

REFERENCE/DOCKET NUMBER: 1122990245

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 727 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHEICAL: no

ANTI-SENSE: no

ORIGINAL SOURCE:

ORGANISM: Gossypium hirsutum

STRAIN: Coker 312

DEVELOPMENTAL STAGE: 10 day old fiber cells

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; TISSUE TYPE: fiber cells
; IMMEDIATE SOURCE:
; LIBRARY: CKB10
; CLONE: B12
US-08-530-797-5

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Query Match 38.1%; Score 259.4; DB 1; Length 727;
Best Local Similarity 72.7%; Pred. No. 6,4e-81;
Matches 335; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

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Oy 220 ATTAGGTCACCTGCGCAACACTTTTCCCTGCACTTGTGCTGCTGCTGCTGCTGCTGCT 279
Db 1 ATAGCGGTACAGCCAGCAACTTTTTCACCTTAATGCTTTATCTAGTACATGCT 60
Oy 280 GGTGTCGAACCTCTCTCTCAACACTTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 339
Db 61 GGTGTCGAACCTCTCTCTCAACACTTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Oy 340 GCTCAATACCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 399
Db 121 GCAGATATCGAGCTGGATGTCCTCTGTATGTTTCAAGAGGTCATGTCAGAAA 180
Oy 400 GGTGAGTGAAGTTTACAAATGATGGCAGCATCTTCAACCTCTTTGATCACAAC 459
Db 181 GGAGGCATCAGGTACACCATGATGAGCAATTCGACTTCAACATGAGGTGATTAACGAC 240
Oy 460 GTGCGTGGCCGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 519
Db 241 GTGGAGAGGGGAGGAGATATACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Oy 520 TCCATGCTGATGAATTTGGGCGCAAACTGCGCAAGCAACTATCTCAATGGCCAAAGC 579
Db 301 CCAATGTCAGAAATTTGGGCGCAAACTGCGCAAGCAACTATCTCAATGGCCAAAGC 360
Oy 580 CTTTCCTTTCAAGTCACTCTTGAAGTGTGCGCACTGCTGCTGCTGCTGCTGCTGCTGCT 639
Db 361 CTCTCTTTTAAAGTACATGCGCAGGATGCGCAGGATGCGCAGGATGCGCAGGATGCGCT 420
Oy 640 TCCAAATGGCAATTTGGCCAAACCTATGAAGGCCCTCAATT 680
Db 421 GCTGCTTGGCAATTCGCAAACTTTTGAAGGAGGCCAGTT 461

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## RESULT 8

US-08-298-829-6

Sequence 6, Application US/08298829

Patent No. 5620882

GENERAL INFORMATION:

APPLICANT: John, Mallyakal E.

TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESS: Nicholas J. Seay, Quarles &amp; Brady

STREET: P.O. Box 2113, First Wisconsin Plaza

CITY: Madison

STATE: Wisconsin

COUNTRY: USA

ZIP: 53701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/298,829

FILING DATE: 19-OCT-1994

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/885,970

FILING DATE: 18-MAY-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/617,239

FILING DATE: 21-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/253,243  
 FILING DATE: 04-OCT-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seay, Nicholas J.  
 REGISTRATION NUMBER: 27,386  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (608) 283-2478  
 TELEFAX: (608) 251-5139  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 727 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Gossypium hirsutum  
 STRAIN: Coker 312  
 DEVELOPMENTAL STAGE: 10 day old fiber cells  
 TISSUE TYPE: fiber cells  
 IMMEDIATE SOURCE:  
 LIBRARY: CKFB10  
 CLONE: B12  
 US-08-298-829-6

Query Match 38.1%; Score 259.4; DB 1; Length 727;  
 Best Local Similarity 72.7%; Pred. No. 6.4e-81;  
 Matches 335; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 220 ATTAGGGTCACTGCGCACAACCTTTTCCCTCTTAATTGGCTCCCTTAACAACAATGGT 279  
 1 ATAAACCGTGACAGCCACCAACTTTTCCCACTAATGCTTTATCTGTGACCAATGGC 60  
 QY 280 GGATGGTGAACCCCTCCCTCCACACTTGCACATGGCTGAGCGCTCCCTTCAATC 339  
 61 GGGTGGTGCATCCCGCAGAGACACTTTGATTTGGCCGACCATCTTGGCGATA 120  
 QY 340 GCTCAATACCGAGCTGGTATCGTCCCGCTCTCTTCTGTAGGGTACCATGATGAAGAA 399  
 121 GCAGAAATATGAGCTGGAATCGCTCCTGTATGTGAGAAGGGTGCATGCTGAAGAA 180  
 QY 400 GTGGAGTAGGTTTACATCAATGAGCCACATCTTCACTGACCTGCTTTGATCAACAAC 459  
 181 GGAGGATCAAGTACACCAATGAATGACATCGTACTTCAACATGGTGTGATGACGAC 240  
 QY 460 GTGGTGGCGCAGGACGTCACATCTGTGTCGATTAAGGGGTCTGCAACTGGATGGCAA 519  
 241 GTGGGAGGGCAGGGGATATTAAGCTGATGATGATGATGATGATGATGATGATGATGAT 300  
 QY 520 TCCATGCTAGAAATTTGGGGCCAAAACCTGCAACAACATCTATCTCAATGGCCAAAGC 579  
 301 CCTATGTCAGAAATTTGGGGCCAAAACCTGCAACAACATCTTAAACGCAAAAGC 360  
 QY 580 CTTTCCTTAAAGCACTCTTAAATGATGTCGACATCTGCTACCTATATATCTCTTCTCT 639  
 361 CTCTCTTTTAAAGTACATGCGACGATGCGACGATGCGACGATGCGACGATGCGACGAT 420  
 QY 640 TCCAAATGGCAATTTGGCCAAACCTATGAAGGCCCTCAATT 680  
 421 GCTGGTTGGCAATTTGGCCAAACCTTTGAAGGAGGCCAGTT 461

RESULT 9  
 US-08-787-335-5  
 Sequence 5, Application US/08787335  
 Patent No. 5981834  
 GENERAL INFORMATION:  
 APPLICANT: John, Maliyakal E.  
 APPLICANT: Umbeck, Paul F.

APPLICANT: Brill, Winston J.  
 TITLE OF INVENTION: GENETICALLY ENGINEERED COTTON PLANTS  
 TITLE OF INVENTION: FOR ALTERED FIBER  
 NUMBER OF SEQUENCES: 18  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Quares and Brady  
 STREET: P.O. BOX 2113  
 STREET: FIRST WISCONSIN PLAZA  
 CITY: MADISON  
 STATE: WISCONSIN  
 COUNTRY: U.S.A.  
 ZIP: 53701  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette - 3.50 inch, 800kb storage  
 COMPUTER: Apple Macintosh  
 OPERATING SYSTEM: Macintosh  
 SOFTWARE: Microsoft Word 4.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/787,335  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/530,797  
 FILING DATE:  
 APPLICATION NUMBER: US 07/253,243  
 FILING DATE: 04-OCT-88  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Nicholas J. Seay  
 REGISTRATION NUMBER: 27,386  
 REFERENCE/DOCKET NUMBER: 1122990245  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 727 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 HYPOTHETICAL: no  
 ANTI-SENSE: no  
 ORIGINAL SOURCE:  
 ORGANISM: Gossypium hirsutum  
 STRAIN: Coker 312  
 DEVELOPMENTAL STAGE: 10 day old fiber cells  
 TISSUE TYPE: fiber cells  
 IMMEDIATE SOURCE:  
 LIBRARY: CKFB10  
 CLONE: B12  
 US-08-787-335-5

Query Match 38.1%; Score 259.4; DB 2; Length 727;  
 Best Local Similarity 72.7%; Pred. No. 6.4e-81;  
 Matches 335; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 220 ATTAGGGTCACTGCGCACAACCTTTTCCCTCTTAATTGGCTCCCTTAACAACAATGGT 279  
 1 ATAAACCGTGACAGCCACCAACTTTTCCCACTAATGCTTTATCTGTGACCAATGGC 60  
 QY 280 GGATGGTGAACCCCTCCCTCCACACTTGCACATGGCTGAGCGCTCCCTTCAATC 339  
 61 GGGTGGTGCATCCCGCAGAGACACTTTGATTTGGCCGACCATCTTGGCGATA 120  
 QY 340 GCTCAATACCGAGCTGGTATCGTCCCGCTCTCTTCTGTAGGGTACCATGATGAAGAA 399  
 121 GCAGAAATATGAGCTGGAATCGCTCCTGTATGTGAGAAGGGTGCATGCTGAAGAA 180  
 QY 400 GTGGAGTAGGTTTACATCAATGAGCCACATCTTCACTGACCTGCTTTGATCAACAAC 459  
 181 GGAGGATCAAGTACACCAATGAATGACATCGTACTTCAACATGGTGTGATGACGAC 240  
 QY 460 GTGGTGGCGCAGGACGTCACATCTGTGTCGATTAAGGGGTCTGCAACTGGATGGCAA 519  
 241 GTGGGAGGGCAGGGGATATTAAGCTGATGATGATGATGATGATGATGATGATGATGAT 300







CURRENT APPLICATION NUMBER: US/09/362,642  
 CURRENT FILING DATE: 1999-07-27  
 NUMBER OF SEQ ID NOS: 8  
 SOFTWARE: Patent In Ver. 2.1  
 SEQ ID NO 1  
 LENGTH: 702  
 TYPE: DNA  
 ORGANISM: Lycopersicon esculentum cv. T5  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (28)..(702)  
 OTHER INFORMATION: tomato expansin (Lex1)  
 US-09-362-642-1

Query Match 36.9%; Score 251.6; DB 4; Length 702;  
 Best Local Similarity 67.2%; Pred. No. 3.4e-78;  
 Matches 391; Conservative 0; Mismatches 179; Indels 12; Gaps 2;

QY 7 GGTGGCTGGCAGAGCGCCACGCCCTTTATGTTGGTGTGACGATCTGGCACCATG 66  
 DB 118 GGTTCATGGGAACCTGACATGTACATTTTACGGCGAAGTGTGCTTCGGAACATG 177  
 QY 67 GGTGGAGCTTGTGGTATGGAATTTATACAGCAAGGATGGCAGCAAGGTGGCG 126  
 DB 178 GGGGTCGTGTGTATGAAATTTATACAGCAAGGATGAGATTAACAGACAGCA 237  
 QY 127 CTGAGCACTGGGCTATTTAACATGATGATTAAGTTGGTGGCTTGCATCGAATGACTGT 186  
 DB 238 CTGAGTACTGTTGTTTAAACATGATGATTAAGTTGGTGGCTTGTGAACTTAATGT 297  
 QY 187 ACAAGACACCT-----AAATGGTCCCTCCGGGAA-----CTATTAGGCTACTGCC 234  
 DB 298 ACAATATCTCTTAATGGAATGTGTCTTCTGGAACCTTCATTTAATCAGAGCT 357  
 QY 235 ACCAATTTGGCCCTCTAATCTTGTCTCCCTAACAAAGATGATGATGTCGAACCTT 294  
 DB 358 ACCAATTTCTCTTAATGGAATGTGTCTTCTGGAACCTTCATTTAATCAGAGCT 357  
 QY 295 CCTCTCCACACTTGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417  
 DB 418 CCTGCTCCCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 477  
 QY 355 GGTATCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 414  
 DB 478 GGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 537  
 QY 415 ACAATCATGGCACTGATCTTCAACCTGTTTGTATCAACAAGCGGTGGCGAGCG 474  
 DB 538 ACCATCATGGATTCCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 597  
 QY 475 GAGCTCCACTCTGTGATGAAGGGGTCTGCACTGGATGCAATTCATGCTAGAAAT 534  
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 QY 535 TGGGGCCAAAAGTGGCAACCACTATCTCAATGGCCAA 576  
 DB 658 TGGGGAACAATTTGGCAATCAATGCGGTTTAACTGTGTCAA 699

RESULT 15  
 US-08-845-539-3  
 Sequence 3, Application US/08845539  
 Patent No. 5929303  
 GENERAL INFORMATION:  
 APPLICANT: Bennett, Alan B.  
 APPLICANT: Rose, Jocelyn K.C.  
 TITLE OF INVENTION: Fruit-specific and Ripening-Regulation  
 TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco

STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/845,539  
 FILING DATE: 25-APR-1997  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bastian, Kevin L.  
 REGISTRATION NUMBER: 34,774  
 REFERENCE/DOCKET NUMBER: 023070-07820005  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 501 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..501  
 OTHER INFORMATION: /product="strawberry faex1"  
 US-08-845-539-3

Query Match 35.7%; Score 242.8; DB 2; Length 501;  
 Best Local Similarity 69.4%; Pred. No. 3.3e-75;  
 Matches 347; Conservative 0; Mismatches 147; Indels 6; Gaps 1;

QY 58 GGCACCATGGGTGAGACCTTGTGGTATGGAATTTATACAGCAAGGATGATGACAGAAC 117  
 DB 1 GGACCATGGGGGGGCTGTGGATATGGAACCTTACAGCAAGGATGATGACAGAAC 60  
 QY 118 AGGATGGCCCTAGACACTGCGCTATTTAACAATGATTAAGTTGGTGGCTTCTTGA 177  
 DB 61 ACTGCTGCCCTAGACAGCGCTCTCTTCAACAATGATGATGATGATGATGATGATGATGAT 120  
 QY 178 ATGACTTGTACAAAGACCTTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 231  
 DB 121 ATCAAGTGGGGGAGAGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 180  
 QY 232 GCCACCACTTTTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 291  
 DB 181 GCCACCACTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240  
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 DB 241 CTTCTCCCGGACCACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
 QY 352 GCTGTATGCTGCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 411  
 DB 301 GCCGATGCTGCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360  
 QY 412 TTTACATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 471  
 DB 361 TTTACATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
 QY 472 GGGGAGTCCACTCTGTGTGATGAAGGGGTCTGGAATGATGATGATGATGATGATGATGAT 531  
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 DB 481 AATTGGGTCAAAGTGGCA 500



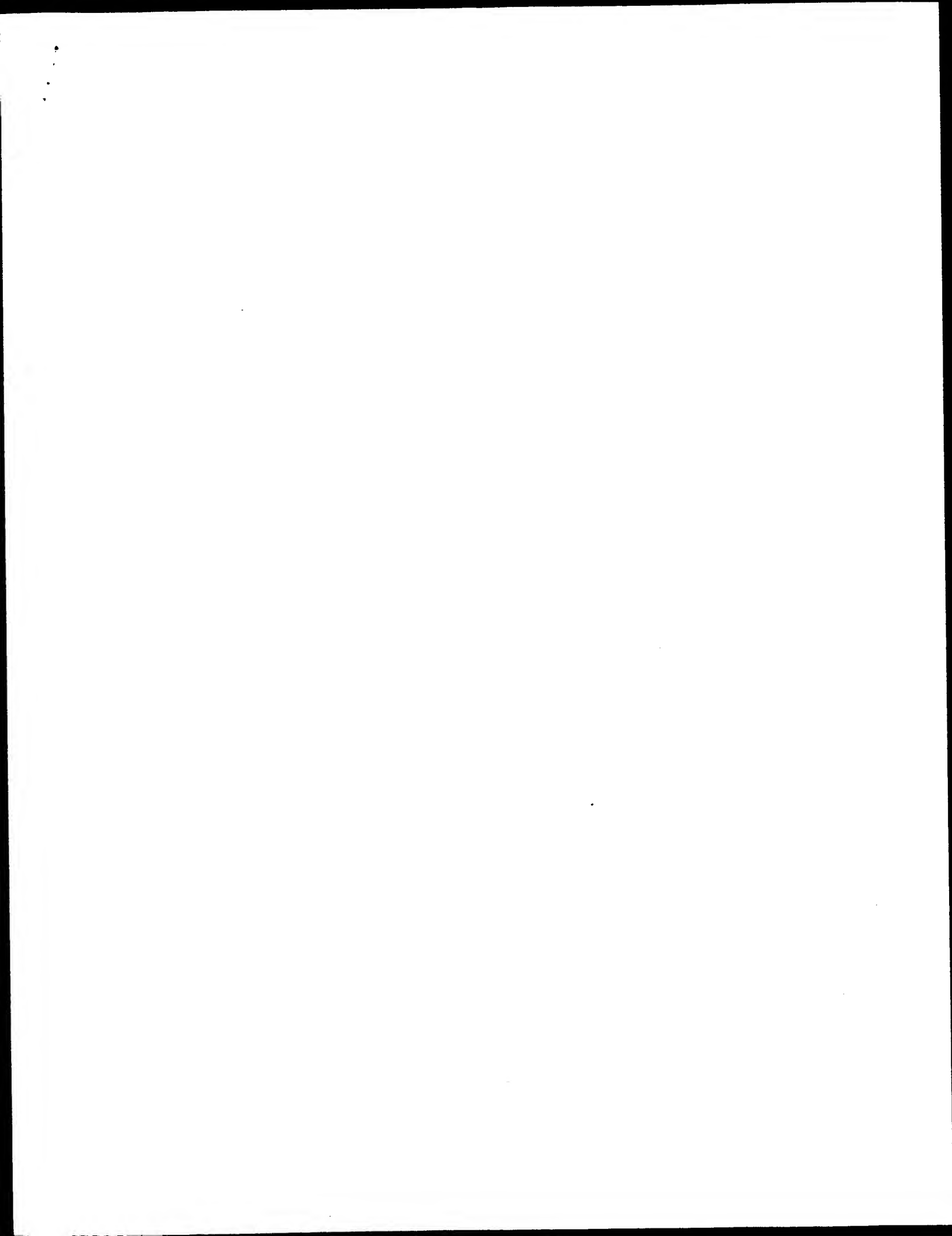
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: October 13, 2002, 18:25:39 ; Search time 244 Seconds

(without alignments)  
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Perfect score: 681  
Sequence: 1 gactacggtgctgcgcagag.....cctatgaagccccaattc 681

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	681	100.0	681	17	AAAT13320
2	392.8	57.7	1015	21	AAAC48712
3	392.8	57.7	1016	21	AAAC40777
4	377.6	55.4	780	21	AAAC50628
5	377.6	55.4	1198	21	AAAC33521
6	377.6	55.4	1233	21	AAAC50633
7	366.6	53.8	1236	21	AAAC40035
8	358.6	52.7	1324	21	AAAC47530
9	353.8	52.0	1326	21	AAAC40169

10	351.4	51.6	1366	21	AAAC47991	Arabidopsis thalia
11	350.2	51.4	1212	21	AAAC45165	Arabidopsis thalia
12	341.6	50.2	1319	21	AAAC44930	Arabidopsis thalia
13	338.2	49.7	1167	22	AAAD03713	Tomato seed expans
14	338	49.6	1205	21	AAAC33121	Arabidopsis thalia
15	331.6	48.7	1201	21	AAAC44975	Arabidopsis thalia
16	316.6	46.5	1236	21	AAAC4714	Arabidopsis thalia
17	313.6	46.0	488	21	AAAC93525	Expansin gene sequ
18	313.4	46.0	824	21	AAAC42473	Arabidopsis thalia
19	312.8	45.9	1213	22	AAAD03711	Tomato seed expans
20	301.2	44.2	1037	21	AAAC42618	Arabidopsis thalia
21	299.4	44.0	1293	21	AAAC37064	Arabidopsis thalia
22	296.2	43.5	1291	21	AAAC50400	Arabidopsis thalia
23	287.6	42.2	475	21	AAAC93526	Expansin gene sequ
24	276.4	40.6	537	20	AAAC68448	Melon expansin Cme
25	262.2	38.5	1103	22	AAAD03712	Tomato seed expans
26	259.4	38.1	727	17	AAAT30255	Cotton fibre cell-
27	259.4	38.1	727	17	AAAT30337	Cotton fibre cell-
28	259.4	38.1	727	18	AAAT70044	Cotton fibre spect
29	259.4	38.1	727	18	AAAT62613	Cotton fibre spect
30	259.4	38.1	727	21	AAAC35549	CDNA sequence a co
31	253.4	37.2	2415	17	AAAT30268	Cotton fibre clone
32	253.4	37.2	2415	17	AAAT3053	Cotton B12 gene an
33	253.4	37.2	2415	18	AAAT70039	Arabidopsis thalia
34	253	36.7	980	21	AAAC41263	Arabidopsis thalia
35	250	36.7	702	20	AAAC68446	Tomato expansin Le
36	242.8	35.7	448	21	AAAC93530	Expansin gene sequ
37	242.8	35.7	501	20	AAAC68447	Strawberry expans
38	222.2	32.6	1132	21	AAAC8981	Arabidopsis thalia
39	218.2	32.0	695	21	AAAC41531	Arabidopsis thalia
40	208.8	30.7	1141	21	AAAC33606	Expansin gene sequ
41	204.6	30.0	437	21	AAAC93528	Expansin gene sequ
42	204.6	30.0	437	21	AAAC93529	Expansin gene sequ
43	177	26.0	1137	21	AAAC47343	Arabidopsis thalia
44	177	26.0	1143	21	AAAC8217	Arabidopsis thalia
45	163.2	24.0	494	21	AAAC93527	Expansin gene sequ

#### ALIGNMENTS

RESULT 1	AAAT13320	standard; DNA: 681 BP.
ID	AAAT13320	
XX	AAAT13320;	
AC	08-JUL-1996	(first entry)
DT		
XX		
DE	Cucumis expansin-29 cDNA.	
XX		
KM	Expansin-29; plant cell wall; cellulose; paper recycling; de-linking;	
KW	polysaccharide; cucumber; ss.	
OS	Cucumis sativus var. Burpee Pickler.	
XX		
PN	AU9540262-A.	
XX		
PD	04-APR-1996.	
XX		
PF	12-MAY-1994;	94AU-0068320.
XX		
PR	12-MAY-1995;	95US-0440517.
PR	12-MAY-1993;	93US-0060944.
XX		
PA	(PENN-) PENN STATE RES FOUND.	
XX		
PI	Cosgrove DJ, McQueen-Mason S;	
XX		
DR	WPI. 1996-201150/21.	
DR	P-PSDB; AAR94527.	
XX		
PT	Expansin proteins which alter the mechanical strength of	

PT poly:saccharide(s) - useful in paper mfr. and recycling  
XX  
PS Disclosure; Page 30; 60pp; English.  
XX  
CC A cDNA clone (AAT13320) codes for cucumber expansin-29 (AA094527),  
CC a member of a novel class of proteins that catalyze the extension of  
CC plant cell walls and the weakening of the hydrogen bonds in pure  
CC cellulose. It was obtd. by PCR amplification of cucumber seedling  
CC cDNA using primers based on isolated peptide fragments of the protein.  
CC The gene can be expressed in bacterial or other systems for use in  
CC recombinant expansin prodn. Expression of the gene in transgenic  
CC plants may allow alteration of plant growth characteristics,  
CC while expression in plant tissue cultures may allow improved prodn.  
XX  
XX  
SQ Sequence 681 BP; 161 A; 179 C; 164 G; 177 T; 0 other;  
  
Query Match 100.0%; Score 681; DB 17; Length 681;  
Best Local Similarly 100.0%; Pred. No. 1.8e-228;  
Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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DB 1 GACTACGGTGGCTGGCAGAGCGGCGACGACCTTTATGCTGCTGCGATCTGGC 60  
QY 61 ACCATGGGTGGAGCTTGTGGTATGGGAATTTATACAGCAAGGATGCGACGACACG 120  
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QY 121 GTGGCGCTGAGACACTGGCGCTATTATACATGATGATTAAGTTGGTGGCTCTTGAATG 180  
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QY 601 AGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660  
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RESULT 2  
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IP AAC48712 standard; DNA; 1015 BP.

XX AAC48712;  
AC 18-OCT-2000 (first entry)  
DT Arabidopsis thaliana DNA fragment SEQ ID NO: 58484.  
DE Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
XX Arabidopsis thaliana.  
XX EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
XX 25-FEB-2000; 2000EP-0301439.  
PF 25-FEB-1999; 99US-0121825.  
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Best Local Similarity 74.4%; Pred. No. 4,1e-127;  
Matches 509; Conservative 0; Mismatches 172; Indels 3; Gaps 1;

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QY 61 ACCATGGGTGAGCGCTTGGCGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGG 120  
DB 221 ACCATGGGTGAGCGCTTGGCGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGG 280  
QY 121 GTGGCGCTGAGCAGCTGCGCTTATTAACAATGATTAATTAATGCTGCTGCTGCTGCTGCTGCTG 180  
DB 281 GCGGCTTTAAGTACGCGCTTATTCACACGAGCTACGAGCTGCGCTGCTGCTGCTGCTGCTGCTG 340  
QY 181 ACTGTACAAACGACCTTAATATGCTGCTTCCGGGAACTATTAGGGTACATGCGCACCAAC 240  
DB 341 AAGTGTACGATGACCCGAGGTGTCTCGGGTCAACCATCACCGTACAGCTACCAAC 400

QY 241 TTTTGGCTTCTACTTGTGCTCCCTACACATGATGGATGNGACACCTCTCTC 300  
DB 401 TTTTGGCCACTTACCTGCTCTCCACGATATGAGTTGGTCAATCTCTCTT 460  
QY 301 CAACACTTGCATGAGTGGCTGCTCTCTCAATAGCTCAATACGAGCTGTATC 360  
DB 461 CAGCATTTGCACTCGCGGAGCCAGCTTTCTCAGATGCTCATGTCGCGGCAAT 520  
QY 361 GTCCCGCTCTCTTCTGTAGGATGATATGATGAAGAGTGTAGGTTTACATC 420  
DB 521 GTTCTGCTCTCTTCCGAAAGATACATGATGAAAGAGGAAATAGGTTTACATC 580  
QY 421 AATGGCCATCTACTTCAACTCGTTTGTATCACAAGCTGCGGCGAGCGAGTC 480  
DB 581 AAGCGACATCTACTTCAACTCGTTTGTATCACAAGCTGCGGCGAGCGAGTC 640  
QY 481 CACTGTGTGATGATGAGGCTCTGAC--TGATGGCAATCATGCTTGAATTTGG 537  
DB 641 CAGGCGCTCTCATCAAGAGCTCAAAACACAGCTGCGAAGCATGCTTGAATTTGG 700  
QY 538 GGCCTCAATCGGCAAGCACTATCTCAATGCGCAAGGCTTCTTCAAGTCACT 597  
DB 701 GGACAAACCTGCGAGCAATCTATCATGACGACCAAGCTTCTTCCAGGTAACG 760  
QY 598 CTAGTATGATGCTGCACTCTCACTGCTATATCTGCTTCTTCAATGCAATTTGGC 657  
DB 761 ACCAGCATGCTGCGACACCTGTTAGCAACGAGCTGCTCTTCAATGCGAGTTCGA 820  
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## RESULT 3

ID AAC40777 standard; DNA; 1016 BP.

XX AAC40777:

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 29509.

XX Hybridisation assay; genetic mapping; gene expression control;

KM protein identification; signal transduction pathway;

KM metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
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PR 01-APR-1999; 99US-0127462.  
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KW metabolic pathway; promoter; termination sequence; ss.
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Query Match	55.4%	Score	377.6	DB	21	Length	1198
Best Local Similarity	72.2%	Pred	No	9.9e-122			
Matches	491	Conservative	0	Mismatches	189	Indels	0
						Gaps	0

Oy	2	ACACGGGTGGCGGAGGCGGACCGACCTTTTATGGGTGGAGCATCTGGCA	61
Db	120	ACGGTGGCGGTTGGATCAACCTCACGCCACTTTTACGGTGGTGGATCTCCGGCA	179
Oy	62	CCATGGGTGGACCTTGGGTATGGGAATTTATACAGCCAAAGGTATGGCAGCAACGG	121
Db	180	CAATGGGTGGTCTTGGATATGGTAATCATTTATACCAAGGCTACGGGACAGCACGG	239
Oy	122	TGGCCCTGAGCAGTCGGCTATTTAAACATGGATTAAGTGGTGGTCTGGCTGCAGATGA	181
Db	240	CGGCTCTAAGCAGACCTCTTCAACATGAGACTTACGTGGTCTTGTGCTTGGAGATAA	299
Oy	182	CTTTGACAAAGACCCCTTAATAGTGCCCTTCCGGGAACCTATTAGGCTACATGCCAACCT	241
Db	300	GATGTGAAGAAAGATGTAAATGTGTATTACCTGGCTCAATGTTGTAAACGCTACAAACT	358
Oy	242	TTTGGCCCTCTTACCTTCTCTCCCTAACAACATGGTGGATGGTGCACACCTCTCTCC	301
Db	360	TCTGCCCCCAATTAACCCGTTAGGAACAATTAATGGCGTGGTGTATCTCTCTCTTG	419
Oy	302	AACACTTGCACATGGCTAGGCTAGCCTGCTCTCTTCAATCGCTCAATACGAGAGCTGTATCG	361
Db	420	AACACTTTGACCTTCTCAGCCTGTGTTTCAACGATTTGCTCAGATACGAGACTGGAAATCG	479
Oy	362	TCCCGCTCTCTTTCGTAGGGTACCATGTATGAAGAAAGGTGAGTGAAGTTTCAATCA	422
Db	480	TCCCGTTTCCACAGGAAGGTTCTCTTCAGAGAGAAAGGAGAAATTAAGATTACAGATAA	539
Oy	422	ATGGGCACTACACTTCAACCTCGTTTGTATCACAAAGCTGGTGGCGCAGGACGACTCC	481
Db	540	ACGGCACTCATACTTCAACTCTGTGTGATGCACAAAGCTGGTGGTCCGGAAACGTTTC	599
Oy	482	ACTGTGTGTCAATAAGGGGTCTCGAACTGATGGCAATCCATGTCTTAGAAATTTGGGGCC	541
Db	600	ACTCGGCGGCGCATCAAGGTTCAAMAGAGTGTGCAAGCATATGTACAAAGGAACGTGGGGGC	655
Oy	542	AAAACGTGCAAGCAACAACATATCTCATGTGGCAAGGCTTTCCTTCAATCTCACTGTTA	604
Db	660	AAAATTTGGAAAGCAACTCTTAACCTCAACGGTCAAGCACTTCTTTAAGGCTCACACCA	719
Oy	602	GTGATGTGTCGCACTCTCACTGCTATTAATCTCGTTCATCTCCAAATTTGGCAATTTGGCCAAA	661
Db	720	GGGAGCGGCGCAGACTGTGTCTCTTCAACGCGCGCTCTGCGGCGTGGCTTATGGCCAGA	775
Oy	662	CCTATGAGAGCCCTCAATTG 681	
Db	780	CTTTTCCGGTGGACAGTTG 799	

## RESULT 6

ID	AAC50633 standard; DNA; 1233 BP.
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AC XX	AAC50633;
DT XX	18-OCT-2000    (first entry)
DE XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 65567 .
KM KM	Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.  
OS OS	Arabidopsis thaliana.
PN PN	EPI033405-AZ.
XX PD	06-SEP-2000.
PF XX	25-FEB-2000; 200EP-0301439.
PR PR	25-FEB-1999;     99US-0121825. 05-MAR-1999;     99US-0123180. PR            09-MAR-1999;     99US-0123548. PR            23-MAR-1999;     99US-0125788. PR            25-MAR-1999;     99US-0126264. PR            29-MAR-1999;     99US-0126785. PR            01-APR-1999;     99US-0127462. PR            06-APR-1999;     99US-0128234. PR            08-APR-1999;     99US-0128714. PR            16-APR-1999;     99US-0129845. PR            19-APR-1999;     99US-0130077. PR            21-APR-1999;     99US-0130449. PR            23-APR-1999;     99US-0130510. PR            23-APR-1999;     99US-0130691. PR            28-APR-1999;     99US-0131449. PR            30-APR-1999;     99US-0132048. PR            30-APR-1999;     99US-0132407. PR            04-MAY-1999;     99US-0132484. PR            05-MAY-1999;     99US-0132485. PR            06-MAY-1999;     99US-0132486. PR            06-MAY-1999;     99US-0132487. PR            07-MAY-1999;     99US-0132863. PR            11-MAY-1999;     99US-0134256. PR            14-MAY-1999;     99US-0134218. PR            14-MAY-1999;     99US-0134219. PR            14-MAY-1999;     99US-0134221. PR            14-MAY-1999;     99US-0134370. PR            18-MAY-1999;     99US-0134768. PR            19-MAY-1999;     99US-0134941. PR            20-MAY-1999;     99US-0135124. PR            21-MAY-1999;     99US-0135353. PR            24-MAY-1999;     99US-0135629. PR            25-MAY-1999;     99US-0136021. PR            27-MAY-1999;     99US-0136392. PR            28-MAY-1999;     99US-0136782. PR            01-JUN-1999;     99US-0137222. PR            03-JUN-1999;     99US-0137528. PR            04-JUN-1999;     99US-0137502. PR            07-JUN-1999;     99US-0137724. PR            08-JUN-1999;     99US-0138094. PR            10-JUN-1999;     99US-0138540. PR            10-JUN-1999;     99US-0138847. PR            14-JUN-1999;     99US-0139119. PR            16-JUN-1999;     99US-0139452. PR            16-JUN-1999;     99US-0139453. PR            17-JUN-1999;     99US-0139492. PR            18-JUN-1999;     99US-0139454. PR            18-JUN-1999;     99US-0139455. PR            18-JUN-1999;     99US-0139456. PR            18-JUN-1999;     99US-0139457. PR            18-JUN-1999;     99US-0139458. PR            18-JUN-1999;     99US-0139459. PR            18-JUN-1999;     99US-0139459.



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Query Match 53.8%; Score 366.6; DB 21; Length 1236;

Best Local Similarity 72.1%; Pred.No.7,4e-118; Mismatches 189; Indels 1; Gaps 1;

Matches 491; Conservative 0;

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DB 160 ACGGTGGCGGTGTGATCAACGCCACGCTTTTACGCTGTGTGATGCTTCCGCA 219  
QY 62 CCATGGGTGAGCTTTGGGTATGGGAATTTATACAGCCAGGATGACCAACCG 121  
DB 220 CAATGGGTGTGCTGTGATATGTAATATATAGCCAGGTAACGAGGACGACG 279  
QY 122 TGGCGCTGAGCACTG-CGCTATTACATGATTAAGTTGGTGGCTTCGTAATG 180  
DB 280 CGGCTCTTAAACAGGSCCTCTTCAACAATGACTTGTGTTCTTCTTGAATA 339  
QY 181 ACTTGTACAACAGCCCTTAATGTCCTTCGCGAACTATTAGGTCACGCAAC 240  
DB 340 AGATGTGAACAGCATGTAATGTGTATTACCGCTCAATGTTGTAACGCTCAAC 399  
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DB 460 GAACTTTGACCTTGTCTAGCTGTTTTCACAGCATTTCTCAGTACGAGCTGAAATC 519  
QY 361 GTCCCGCTCTCTTGTGAGGATACCATGTATGAAGAAAGTGAGTGAGTTTCAATC 420  
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QY 421 AATGGCCTCATCTTCAACCTCGTTTGTATCAAAAGTGGTGGCGAGGACGTC 480  
DB 580 AACGGCCACTCATCTTCAACCTTGTGATCAAAAGGTGGTGGCGGAGACGCTT 639  
QY 481 CACTGTGTGATTAAGGGGTCTGCACTGATGATGCAATTCATAGAAATTTGGGAC 540  
DB 640 CACTGCGCGCGCATCAAGGCTTCAAGACAGTGTGCAAGCATATGTCAAGAACTGGGG 699  
QY 541 CAATCTGCAAAAGCAACATATCTCATGAGCGCTTCTTCACTCACTCTT 600  
DB 700 CAATATTTGCAAAAGCAACATCTTCACTCAAGGCTTCTTCAAGTCAACACC 759  
QY 601 AGTATGTCGACACTCTGCTATTAATCTGTTCTTCAATTTGCAATTTGGCCAA 660  
DB 760 AGGACGCGCGACACTTCTCTTCAAGCGCTGCTGCGGCTGTATATGCGCAG 819  
QY 661 AACTATGAAGGCGCTCAATTC 681  
DB 820 ACTTTTGGCGGTGACAGCTTC 840



RESULT 8  
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DT 18-OCT-2000 (first entry)  
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XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
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XX  
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KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
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XX  
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QY 127 CTGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 186
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Query Match 50.2%; Score 341.6; DB 21; Length 1319;  
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DB 291 GGGAGAGCTTGGGTATGGATTTATACAGCAAGGGTATGGCAGCAACACGCGTGC 350
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DB 411 GCGCAGACACCTCAATGTCACCTCACTGAGTGTCTTTCGATCTCATACCGCAACCA 470
QY 240 CTTTGGCCCTCTTAATTTGGCTCCCTTAACACAAATGATGATGTCACCTCTCT 299
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QY 360 CGTCCCGCTCTCTTGTGTAGGTAACATATGTAAGAAAGCTGATGAGTTAAT 419
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QY 480 CCACTCTGTGCATPAAAGGCTCTGCACTGATGCAATCATGTCTAGAAATTTGGG 539
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DB 891 AACCTTGTGCGAAGAAATTTTC 912

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## RESULT 13

AAD03713 standard; cDNA; 1167 BP.

AAD03713:

19-JUN-2001 (first entry)

Tomato seed expansin, *LeEXP10*, cDNA for controlling seed germination.

Tomato: endo-beta-mannanase; Lycopersicon esculentum mannanase2; LEMMN2;  
 polyglacturonase; PG; LeEXP1; cellulase; arabinosylase; LeEXP1;  
 xyloglucan endotransglycosylase; XET; LeEXP4; expansin; LeEXP8;  
 LeEXP10; hydrolase; endosperm cap; tissue weakening; radicle growth;  
 seed germination; ss.

Lycopersicon esculentum.

Key Location/Qualifiers  
 CDS 85..837  
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 /product= "Tomato seed expansin, *LeEXP10*"

W0200123530-A1.

05-APR-2001.

29-SEP-2000; 2000MO-US26884.

30-SEP-1999; 99US-0410191.

(RBGC ) UNIV CALIFORNIA.

Bradford KJ, Chen F, Dahal P, Downie B, Nonogaki H;

XX WPI: 2001-266144/27.  
DR P-PSDB; AAE00414.  
XX Novel nucleic acid sequences isolated from germinating seeds encoding  
PT polypeptides that are useful to control seed germination in plants  
XX  
PS Claim 4: Page 50; 63pp; English.  
XX  
CC The present invention relates to enzymes such as seed-specific  
CC endo-beta-mannanase (e.g., Lycopersicon esculentum (Le) MAN2),  
CC polygalacturonase (PG) (e.g., LEXP1), cellulases such as Cel55 and  
CC Cel68, arabinosidase (e.g., LeAR), xyloglucan endotransglycosylases  
CC (XET) (e.g., LEXET4) and expansins such as LEXXP4, LEXXP8 and LEXXP10  
CC isolated from germinating seeds. All these enzymes are expressed  
CC initially in the endosperm caps and are associated with cell wall  
CC hydrolysis. These enzymes are associated with weakening of tissues  
CC surrounding the embryo and/or initiating radicle growth. The control of  
CC expression of these endogenous genes is therefore a convenient means for  
CC controlling seed germination. The present sequence is tomato seed  
CC expansin, LEXXP10, cDNA. Expansins are extracellular proteins that  
CC facilitate cell wall extension.  
XX  
SQ Sequence 1167 BP; 319 A; 184 C; 268 G; 396 T; 0 other;

Query Match 49.7%; Score 338.2; DB 22; Length 1167;  
Best Local Similarity 69.0%; Pred. No. 6.8e-108;  
Matches 463; Conservative 0; Mismatches 208; Indels 0; Gaps 0;

QY 10 GCGTCGACGAGCGCCACCCCTTTATGTTGGTGAGCCATCTGGCACCATTGGT 69  
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DB 220 GGAGCATGTGTTATGGATTTGTACAGTGAAGATATGTTACAAACAGAGCATTTG 279  
QY 130 AGCATTGCGCTATTTAAACAATGATTAGTTGGTCTTCTTCAAAATGACTTTGATA 189  
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DT 17-OCT-2000 (first entry)  
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KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
XX metabolic pathway; promoter; termination sequence; ss.  
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PN EP1033405-A2.  
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PF 25-FEB-2000; 2000EP-0301439.  
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PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
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GenCore version 5.1.3  
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DEFINITION Sequence 1 from patent US 5959082.  
ACCESSION AR076514  
VERSION AR076514.1 GI:10003260  
KEYWORDS  
SOURCE  
ORGANISM Unknown.

REFERENCE  
1 (bases 1 to 681)  
AUTHORS Cosgrove,D.J., McQueen-Mason,S., Gullinan,M., Shcherban,T. and Shi,J.  
TITLE Proteins catalyzing the extension of plant cell walls  
JOURNAL Patent: US 5959082-A 1 28-SEP-1999;  
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DEFINITION Sequence 1 from patent US 6255466.  
ACCESSION ARI61478  
VERSION ARI61478.1 GI:16227385  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 681)  
AUTHORS Cosgrove,D.J., McQueen-Mason,S., Gullitman,M., Shcherban,T. and Shl,J.  
TITLE Purified plant expansion proteins and DNA encoding same  
JOURNAL Patent: US 6255466-A 1 03-JUL-2001;  
FEATURES  
Source location/Qualifiers  
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DEFINITION Sequence 1 from Patent WO0188163.  
ACCESSION AX306490  
VERSION AX306490.1 GI:17645710  
KEYWORDS  
SOURCE Cucurbit.  
ORGANISM Cucumis sativus

REFERENCE 1 (sites)  
AUTHORS Berendes,F., Rast,H.G., Vogt,U. and Gouloudis,C.  
TITLE Method for producing recombinant expansins  
JOURNAL Patent: WO 0188163-A 1 22-NOV-2001;  
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481 CACTGTGTGATTAAGGGGTCTCGAAGTGGATGCAATCATGTCTAGAAAATGGGCG 540  
481 CACTGTGTGATTAAGGGGTCTCGAAGTGGATGCAATCATGTCTAGAAAATGGGCG 540  
541 CAAACTGCGCAAGCAACATATCTCAATGCGCAAGCGCTTTCCTTCAAGTCACTCTT 600  
541 CAAACTGCGCAAGCAACATATCTCAATGCGCAAGCGCTTTCCTTCAAGTCACTCTT 600  
601 AGTATGATGGGCACTCTCACTGCTATATATCTGCTTCTTCAATTTGGCCAA 660  
601 AGTATGATGGGCACTCTCACTGCTATATATCTGCTTCTTCAATTTGGCCAA 660  
661 ACCTATGAGAGCCCTCAATTC 681  
661 ACCTATGAGAGCCCTCAATTC 681

RESULT 4  
CSU30382 992 bp mRNA linear PLN 04-DEC-1996  
LOCUS Cucumis sativus expansin (Cs-Exp1) mRNA, complete cds.  
DEFINITION  
ACCESSION U30382  
VERSION U30382.1 GI:1040874  
KEYWORDS

SOURCE

ORGANISM cucumbers.  
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Cucumls.  
1 (bases 1 to 992)  
Sheherban, T.Y., Shi, J., Durachko, D.M., Gullitman, M.J.,  
McQueen-Mason, S.J., Shieh, M., and Cosgrove, D.J.  
Molecular cloning and sequence analysis of expansins--a highly  
conserved, multigene family of proteins that mediate cell wall  
extension in plants  
Proc. Natl. Acad. Sci. U.S.A. 92 (20), 9245-9249 (1995)  
66016146  
2 (bases 1 to 992)  
Sheherban, T., Shi, J., Durachko, D.M., Gullitman, M.J.,  
McQueen-Mason, S.J., Shieh, M., and Cosgrove, D.J.  
Direct Submission  
Submitted (27-JUN-1995) Daniel J. Cosgrove, Biology, Pennsylvania  
State University, 208 Mueller Laboratory, University Park, PA  
16802, USA

FEATURES

source location/Qualifiers  
1..992  
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223..903  
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992  
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/note="17 A nucleotides"  
BASE COUNT 259 a 277 c 177 g 279 t

ORIGIN

Query Match 100.0%; Score 681; DB 8; Length 992;  
Best Local Similarity 100.0%; Pred. No. 8.9e-199;  
Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GACTACGGTGGCTGCGAGACGGCCACGCTTTTATGTGGTGGTACGACATCTGCG 60  
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223 GACTACGGTGGCTGCGAGACGGCCACGCTTTTATGTGGTGGTACGACATCTGCG 282  
223 GACTACGGTGGCTGCGAGACGGCCACGCTTTTATGTGGTGGTACGACATCTGCG 282  
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121 GTGGCGGTGACGACGTGGCTATTTACAAATGATTAAGTTGTGGTCTTGTCCGAATG 180  
121 GTGGCGGTGACGACGTGGCTATTTACAAATGATTAAGTTGTGGTCTTGTCCGAATG 180  
343 GTGGCGGTGACGACGTGGCTATTTACAAATGATTAAGTTGTGGTCTTGTCCGAATG 402  
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403 ACTTGTACAAAGACCCCTAATGATGTCCTCCGGAATATTAGGCTACCTGCGACCAAC 462  
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241 TTTTGGCCCTCTTAACCTTGTCTCCCTACCAACATGTGGATGGTGGCAACCTCTCTC 300  
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CDS		74.. 838 /gene="PA-Expi" /product="expansin" /codon_start=1 /protein_id="AAC31529.1" /db_xref="GI:3510538" /translation="MAPOLSLAPLALSLVLENLHLHGAFAADYGSMEGAHATFYGGDD ASTMGACAGCYNLYSOGVYNTFALSTALFNNGLSCGSCYEMRCNNDPRMCRPSII VIRINFCPPNPASNDNSGNPNLHOFHDLAEPAFIOAYRAGIYPTVFRVDMKMK GGRLEFINHSTFNLVLTNNYGAGADYHASTIGSRFTGMQPHSRMGMQMSNNYLNIG OSLSFVYTSIDERTVSTYNVAPGMQDVGOTFSSGQF"
BASE COUNT	301 a 254 c 242 g 312 t	
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Best Local Similarity	77.8%;	Pred. No. 6.2e-124;
Matches 529; Conservative	0; Mismatches 151;	Indels 0; Gaps 0;
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155	GATTATGGTGGCTGGGAAGGGCCATGCACATTTTATGCTGTGCGGTGATGCCTCGGA	214
61	ACCATGGGTGAGCTTGTGGTATGGAAATTTATACAGCCAGGGTATGACGACACAGC	120
215	ACCATGGGGGAGCATGTGGGTATGGGAACCTTTATACGCAAGGGTATGAGAACCAACT	274
121	GTGGGCGTGAGACATGCGCTATTAAACAATGATTAAGTTGTGCTTCCTTGGAAATG	180
275	GCAGCTTTTAAGCACAGCCTTCTTAACAATGGCTTGAGCTGTGGCTTGTATGAAATG	334
181	ACTTGACAAAGACCCCTAAATGTGCTTCCGGGAACCTTATAGGGTACATGCGCACAC	240
335	AGATGCACAATGACCTTAGATGTGTGCTGTGGAAGCATCTTGTATCTGCCAACAC	394
241	TTTTGGCCCTCAACTTTGTCTCCCTCAACAACAAGTGTGATGAGTGCACACCTCTTC	300
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301	CAACACTTGACATGGCTGAGGCTGCTCTTCAAAATCGCTAATACGAGACCTGGATTC	360
455	CAGCAGCTTGAATTTGGCTGAGGCTGCTCTTCTTAATTTGCCAATACGCGCTGGGATT	514
361	GTCCCGCTCTCTTTCGTAGAGGTATCATGATGTAAGAAAGTGGAGTGAAGTTTCAATC	420
515	GTGCTGTATCACTTCAGAGAGTGGCCCTGTATGAAGAAGGAGGAATCAGATTTACCATC	574
421	AATGGCAGCTACTACTTCAACCTCGTTTGTATCAACAACGTGGTGGCGCAGCGACGTC	480
575	AATGGCAGCTCACTTCAACTGGTTTGTATCAACAACGTGGTGGTGGTGGAGGACGTC	634
481	CACCTGTGTGATTAAGGGGTCTGGAACGTGGATGGGAATCATGTTTCAAAATTTGGGCG	540
635	CACCTCACTTTCATCAAGGGGGTCCAGAAAGGGTGGGACCAACCATGTACAGAACTGGGG	694
541	CAAAAGTGGCAAGCAACAATATCTCAATGAGCCCAAGGCGCTTCTTTCAGTCACTTT	600
695	CAAAAGTGGCAAGCAACAATTAACGTCAATGGCCAGACCTCTCTTCCAAAGTCACACC	754
601	AGTAGGTGCGACCTCAGCTGCTTATATCTCGTTCCTTCCATATGGCAATTTGGCCAA	660
755	AGTAGCGGAAGAACTGTTACAAACCTTCAACGTCGGGCGCTGGTAAATGTGCAAGTTGGTCA	814
661	ACGTATGAAGGCCCTCAATT	680

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Db      B15 ACTTTCACAGGGGCTCAATT 834          ||| ||| |||||
RESULT 7
CAR291817 CAR291817 1035 bp mRNA linear PLN 19-DEC-2000
LOCUS Cicer arletium mRNA for expansin, clone CanExp-2.
DEFINITION AJ291817
ACCESSION AJ291817 GI:11932091
VERSION expansin.
KEYWORDS chickpea.
SOURCE Cicer arletium
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Cicereneae;
Cicer.
REFERENCE 1 (bases 1 to 1035)
AUTHORS Duplico,B., Sanchez,M.A. and Labrador,E.
TITLE An second expansin is expressed in chickpea epicotyls
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1035)
AUTHORS Labrador,E.
TITLE Direct Submission
JOURNAL Submitted (15-DEC-2000) Labrador E., Dpto. Fisiologia Vegetal,
Univ. Salamanca, Campus Miguel de Unamuno. Pza. Doctores de la
Reina s/n, E-37007, SPAIN
FEATURES
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VPCKRKGGIRFTINGHSIFNLVLVTNNGAGDVHSVSIKGSRTQMOSRMHGOMOS
NSYLNGOPLSFQVTVTSDEKMTSTINVAAPSMMOFGOTRGAGP"
BASE COUNT   312 a    168 c    213 g    342 t
ORIGIN
Query Match           63.7%: Score 433.6; DB 8; Length 1035;
Best Local Similarity 77.4%; Pred. No.1,9e-122;
Matches 526; Conservative 0; Mismatches 154; Indels 0; Gaps 0;
 Oy      1 GACTACGGTGCTGCGAGAGCGGCCACGCCACCTTTTATGCTGCTGTCAGCATGTGGC 60
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 Db      129 GATTATGGTGTGGAGGCGTCCAAAGCCAATTTCTATGTTGGGTGATGCTTGGC 188
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 Db      189 ACAATGGGTGAGCATGTGGATATGGTAATTTGTAATAGCCAGAAGTATGGACAACACACA 248
 Oy      121 GTGGCGCTGACGACTGCGCTTTTAAACAATGATTAAGTGTGCTTGCCTTGCGAANTG 180
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 Db      249 CGAGCACTAACGACACTGTTTATTCACAACATGTTTAGTGTGATCTTCTATGAANAATG 308
 Oy      181 ACTTGTACAACAGACACCCTAATGGTGGCTTCGGGAAGTATTAAGTGCACATGCGACCAAC 240
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 Db      309 ACATGCATGATGATCCAAAGATGGGCAACACCTGGCTCTATATTGTTACTGCCACAANAAT 368
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 Db      369 TTTTGCACCAANAATGCATCTTTGGCTAATAATAGCTGGTGTGTTGTAACCCCTCTTGG 428

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[illegible]

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus. 1 (bases 1 to 1048)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Wu, Z. and Miersma, P.A.  
Differential Expression of Expansin Genes Isolated from Sweet Cherry (Prunus avium L.) During Fruit Ripening  
Unpublished  
2 (bases 1 to 1048)  
Wu, Z. and Miersma, P.A.  
Direct Submission  
Submitted (18-AUG-2000) Agriculture and Agri-Food Canada, Pacific Agri-Food Research Centre, 4200 Highway 97, Summerland, British Columbia V0H 1Z0, Canada  
Location/Qualifiers

FEATURES  
source

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BASE COUNT 281 a 245 c 234 g 288 t  
ORIGIN

Query Match 62.7%; Score 427.2; DB 8; Length 1048;  
Best Local Similarity 76.8%; Pred. No. 1,8e-120;  
Matches 522; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 1 GACTACGGTGGCTGGAGAGCGGCGACACCTTTATGATGCTGACGATCGGC 60  
DB 162 GATTATGCTGGCTGGAGAGCGGCGATCCATCTTTATGCTGCGGTGATGCTCGGA 221  
QY 61 ACCATGGCTGGAGCTTGGTATGGATTTATACAGCCAGGATATGGCAGAACACG 120  
DB 222 ACAATGGGGGAGCATGTGGTATGGACCTTGACAGCCAGGATATGGACCAACACT 281  
QY 121 GTGGCGCTGAGCACTGGCTATTAAACAATGATTAAGTGTGCTGCTTGAATG 180  
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QY 181 ACTTGTACAAGACCTTAATGCTGCTTCCGGAACTATAGGCTCACTGCCACAC 240  
DB 342 AGATGCAACAATGACCTTAGATGTGCTGCGTGAAGCATCATTTGTACTGTACAAAC 401  
QY 241 TTTTGGCTCTCAATTTGCTGCTCCCTAACAAATGATGATGATGCAACCTCTCTC 300  
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DB 462 CAGCACTTTCATTTGGCGGAGCTGCTTCTTCAATATGCCAATACCGCGTGGATT 521  
QY 361 GTCCCGCTCTCTTGGTATGAGGATGATGATGATGATGATGATGATGATGATGAT 420  
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QY 481 CACTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540

DB 642 CATTACGTTTCATCAAGGATCCAGAACAGGCTGGCAACCCATGTCACAAAGAACTGGGG 701  
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QY 601 AGTATGCTGCGCACTGCTCACTGCTTATCTGCTTCTTCAATGCGCAATTTGGCCAA 660  
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RESULT 10  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Prunus cerasus.  
Prunus cerasus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus. 1 (bases 1 to 1109)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Yoo, S.-D., Gao, Z., Cantini, C., Loeschner, W. and van Nocker, S.  
Coordinated expression of genes encoding expansins and other cell wall-modifying enzymes is associated with pectin-related changes in the cell wall during ripening of cherry (P. cerasus) fruit  
Unpublished  
2 (bases 1 to 1109)  
Yoo, S.-D. and van Nocker, S.  
Direct Submission  
Submitted (19-FEB-2001) Department of Horticulture, Michigan State University, 392A Plant and Soil Science Building, East Lansing, MI 48824, USA  
Location/Qualifiers

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BASE COUNT 308 a 251 c 239 g 311 t  
ORIGIN

Query Match 62.7%; Score 427.2; DB 8; Length 1109;  
Best Local Similarity 76.8%; Pred. No. 1,8e-120;  
Matches 522; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 1 GACTACGGTGGCTGGAGAGCGGCGACACCTTTATGATGCTGACGATCGGC 60  
DB 136 GATTATGCTGGCTGGAGAGCGGCGATCCATCTTTATGCTGCGGTGATGCTCGGA 215  
QY 61 ACCATGGCTGGAGCTTGGTATGAGGATGATGATGATGATGATGATGATGATGATGAT 120  
DB 216 ACAATGGGGGAGCATGTGGTATGAGCACTTGTACAGCCAGGGGTATGAGCAACACT 275

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OY	181	ACTGTGACAAACGACCCTTAATATGGTCCCTCCGGGAACTATTAGAAGTCACTGCCAACAC	240
Db	336	AGATGCAACAATATGACCTAGATGGTGTGCTCTGGAAACATCATATGTATCTGTAACAAC	395
OY	241	TTTTGCCCCTCTAACTTTGCTCTCCCTAACACAACATGCTGATGGTGTGAACCTCTCTC	300
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OY	301	CACACACTCCGACATGGGCTGAGACCTGCCCTTCCTCAATACGCTCAATACGAGCTGGATTC	360
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OY	361	GTCCCCCTCTCTCTTCTGAGGGATACCATGATATGAAGAAGGTGAGTAGGTTTACAATC	420
Db	516	GTGCTGTATTACTTTCAGAAAGTGGCCCTGTATGAAGAAGGAGAAATAGATTCCACATC	575
OY	421	AATGGCCACTCATATCTTAACCTCGTTTTGATCACAAACGTGCGGTGGCGAGCGACCTC	480
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Db	636	CATTACGTTTCAITATAGAGGATCCGAACAGGGTGGGACCAACCATCTCAAGAAACGTGGGG	695
OY	541	CAAACTGGCAAGACACAACTATCTCAATGGCCCAAGGCTTTCTCTTCAAGTCACTCTT	600
Db	696	CAAACTGGCAGAGACACACTACTCTCAATGGCCAGAGCCTCTCTTCCAAATGAGTACAC	755
OY	601	AGTATATGTCGACACTCTACATGCCATATATCTGCTTCCATATGGCAATTTGGCCAA	660
Db	756	AGTGACGGAAAGACGTGTACAACAACGTGGCCCTCGTATATTTGGCATTTTGCTCAG	815
OY	661	ACCTATGAAGGCCCTCTCAATT	680
Db	816	ACTTCTCAGGGGGTCAATT	835
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DEFINITION	Prunus cerasus expansin (EXPL) mRNA, complete cds.		PLN 01-MAY-2001
ACCESSION	AF350936		
VERSION	AF350936.1	GI:13898648	
KEYWORDS	.		
SOURCE	Prunus cerasus.		
ORGANISM	Prunus cerasus.		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
TITLE	Rosidae; eurosids I; Rosales; Rosaceae; Amygdaloidae; Prunus.		
	1 (bases 1 to 1233)		
	Yoo,S.-D., Gao,Z., Cantini,C., Loescher,W. and van Nocker,S.		
	Coordinated expression of genes encoding expansins and other cell		
	wall-modifying enzymes is associated with pectin-related changes in		
	the cell wall during ripening of cherry ( <i>P. cerasus</i> ) fruit		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1233)		
AUTHORS	Yoo,S.-D. and van Nocker,S.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-FEB-2001) Department of Horticulture, Michigan State		
	University, 392A Plant and Soil Science Building, East Lansing, MI		
	48824, USA		

FEATURES	
source	Location/Qualifiers
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BASE COUNT	327 a 253 c 302 g 351 t	
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Query Match	61.8%; Score 420.6; DB 8;	Length 1233;
Best Local Similarity	76.4%; Pred. No. 1,9e-118;	
Matches 516; Conservative	0; Mismatches 159; Indels 0; Gaps 0;	
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Oy	67	GCTGAGCCTTGTGGTATGGAATTTATACGCCAACGAGGTATGGCACGAAACACGGTGGC 126
Db	201	GGAGGTGCTTGTGGATATATGAAATTTGATATGCCAAGGATATGGAAACCATGCACTGACGT 260
Oy	127	CTGAGCACTGCGCTATTTACAAATGATTAAGTTGTGTGTCTTGCCTTGCAAATACCTTGT 186
Db	261	CTCAGCACAGCTCTGTTCAACGATGGCTTGAGCTGTGGGTATGTTATGAGATGAGATGT 320
Oy	187	ACAAGCACCCCTAAATGTTGGCTTCCGGGACACTATTAGAGGTGCTGCCCACCAACTTTTGC 246
Db	321	GACAGTAGCCCCAATATGTTGGCTTCCCGGACGACATCATGTCACATGCCCAACACTTTCG 380
Oy	247	CCTCCTAACTTTGCTCTCTCCCTPAACAAACATGTGTGATGTGTCAACCTCTCTCCACAC 306
Db	381	CCTCCTAACTTAGCTCACTTAATGACATGATGTGATGTGTCAACCTCTCTCCACAGAC 440
Oy	307	TTCGACATGGTGGCCGCTCCTCTCCAATTCGCTCAATACCGACGTGATGCTGCC 366
Db	441	TTTGATTTGGCTGAGCCCTGCTCTTCTTCAAAATGTCTCAATACCGACGTGGAATTTGCC 500
Oy	367	GTCCTCTTTGCTAGGGTACATGTAAGAAGAAAGGTGAGTGAAGTTTACAAATCAATGGC 426
Db	501	GTCCTCTTACAGAGGTTCTTGTGTGAAGAAAGGAGGATTAAGATTCACCGTCAACCGT 560
Oy	427	CACATATACCTTACCTGTTTTATTCACAAACCTCGGTGGCGGAGGAGTCCACTCT 486
Db	561	CACCTTACTTCACTTGGTTTGTATGATCAACACGTTGAGGGTGAAGGATGTGCACACTCT 620
Oy	487	GTCGTGATAAAGGGGTCTCGAACTGATGGCAATCATGCTTGAATAATTTGGGGCCAAAAC 546
Db	621	GTTTCAATCAAGGGGTCCAAAACGAGGTGGCAAGCCATGTCAAAGAACCTGGGGCCAGAAC 680
Oy	547	TGGCAAGCACACTATCTCATGTGATGGCCCAAGGCCCTTCTCTTCAAGTCACTTTAGTAT 606
Db	681	TGGCAGAGCAACTCTTACTCTCAATGGCCAGGCTCTGTCTTTCACAGTCAACCACTGAC 740
Oy	607	GSTGCACTGCTACTGCGCTATATGCTGCTCTTCCAAATTTGCACAAATGACCAATCTAT 666
Db	741	GGTAAAGCTGTACCAACGACCAATGCTGTGTCAGCTGACTGACATTTGGTGAACAACTTT 800
Oy	667	GAAAGCCCTCAATTC 681
Db	801	TCGGGGGCTCAATTC 815
RESULT 12		
AF159563	1180 bp	mRNA linear PLN 30-DEC-1999
LOCUS		
DEFINITION	Fragaria x ananassa expansin (Exp2) mRNA, complete cds.	
ACCESSION	AF159563	
VERSION	AF159563.1	GI:6646884



KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

*Fragaria x ananassa*.  
*Fragaria x ananassa*.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eustroids I; Rosales; Rosaceae; Rosoidae; *Fragaria*.  
1 (bases 1 to 1180)  
Civello,P.M., Sabehat,A., Powell,A.L.T. and Bennett,A.B.  
An expansin gene expressed in ripening strawberry fruit is  
auxin-independent  
Plant Physiol. 12 (4), 1273-1279 (1999)  
2 (bases 1 to 1180)  
Civello,P.M., Sabehat,A., Powell,A.L.T. and Bennett,A.B.  
Direct Submission  
Submitted (16-JUN-1999) Dept. of Vegetable Crops, Univ. of Calif.  
Davis, Mann Lab, Davis, CA 95616, USA  
Location/Qualifiers  
1..1180  
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/gene="Exp2"  
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BASE COUNT 292 a 262 c 290 g 336 t  
ORIGIN

Query Match 61.3% Score 417.6; DB 8; Length 1180;  
Best Local Similarity 75.9%; Pred. No. 1.6e-117;  
Matches 516; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 2 ACTACGGGTGGAGAGCGGCGACGCACTTTATGAGTGTGTCGACGATCGCA 61  
DB 124 ACGGCGCGGTTGGTTGGCCATGTCATTTATGAGAGTGTGTCGTCGCA 183  
QY 62 CCATGGGTGAGCTTGTGGTATGGAATTTATACAGCCAGGCTATGCGACGAC 121  
DB 184 CAATGGAGGTGATGTGATGAACCTTGTACAGCCAGGCTATGACCAACACTG 243  
QY 122 TGGCGGTGAGCACTGGCTATTATTAACATGATTAAGTGTGTCGTCGCAATGA 181  
DB 244 CAGCACTTAAGCAGACGCTCTTCAACGATGCTTGAGCTGCGGCTTCTTACGAATGC 303  
QY 182 CTGTGACAAACGACCTTAATGCTGCTTCGCGGAATTTAGGCTCACTGCGCAACT 241  
DB 304 GATGTGACATGACCTAGATGCTGCTTCGCGGAATTCATGTCAGCGCACCAACT 363  
QY 242 TTTGGCCCTCTAATCTGTCTCCCTAACACAAAGTGTGATGTCACCTCTCTGC 301  
DB 364 TCTGCCCTCCCACTTGTCTGACGGCAATGACAGCGTGTGTCACACCTCCCTCC 423  
QY 302 AACACTTGCACATGCTGAGCTGCTGCTTCAATGCTCAATGCTCAATGCTGATGCG 361  
DB 424 AGCACTTGATTTTGGCGGAGCTGCTGCTTCAATGCTCAATGCTGATGCGTGTATG 483  
QY 362 TGGCGCTCTCTTCTGATGAGGATGATGATGAAGAGTGTGATGATGATGATGAT 421  
DB 484 TCCCGCTCTCATTCAGAAAGTGTGCTGTGTGTAAGAGGAGGATGATGATGATGAT 543  
QY 422 ATGGCACTCATCTCAACCTGTTTGTATGACAAAGTGTGTCGCGGAGCGGACGTC 481

DB 544 ACGGCACTTCTACTTCAACTTGTTTATGATCACAAGCTTGACAGACAGATGTC 603  
QY 482 ACTGTGTCTCAATAAGGGTCTCGAAGTGCATTCATGTAATAATGGGCC 541  
DB 604 ACTCGGTTTCGATCAAGAGCTTCAAGGGTGTGTCATTCATGTAAGAGTGGGAC 663  
QY 542 AAACTGGCAAGAACAACTATCTCATGTCGCAAGGGCTTCTTCAATGCTCTTA 601  
DB 664 AGAATGCGACAGCAACACTACTCTCAACGACAAAGCCCTGTTTCAAGTCAACCA 723  
QY 602 GTGATGTGCGCACTCTCACTGCTTAAATCTGTTCTTCAATTTGGCAATTTGGCANA 661  
DB 724 GTAGCGGAGGAGCTGTGACAGCAACAGCTTGGCCCTGTAACGCGATTTGGTCAAA 783  
QY 662 CCTATGACGGCCCTCAATTC 681  
DB 784 CTTTTCAGGGCGGTCAATTC 803

RESULT 13  
AF096776 1147 bp mRNA linear PLN 26-OCT-2000  
LOCUS AF096776  
DEFINITION Lycopersicon esculentum expansin (leexp2) mRNA, complete cds.  
ACCESSION AF096776  
VERSION AF096776.1 GI:3747131  
KEYWORDS  
SOURCE tomato.  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asterales; easterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
1 (bases 1 to 1147)  
Catala,C., Rose,J.K.C. and Bennett,A.B.  
Auxin-regulated genes encoding cell wall-modifying proteins are  
expressed during early tomato fruit growth  
Plant Physiol. 122 (2), 527-534 (2000)  
JOURNAL MEDLINE 20144019  
PUBMED 10677445  
REFERENCE 2 (bases 1 to 1147)  
Catala,C., Rose,J.K.C. and Bennett,A.B.  
Direct Submission  
Submitted (02-OCT-1998) Vegetable Crops, University of California  
Davis, Davis, CA 95616, USA  
Location/Qualifiers  
1..1147  
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VTYSNNVAPENMFQGFSSGQP"

BASE COUNT 312 a 208 c 235 g 392 t  
ORIGIN

Query Match 60.98% Score 414.4; DB 8; Length 1147;  
Best Local Similarity 75.6%; Pred. No. 1.6e-116;  
Matches 514; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 1 GACTACGCTGCTGCGAGCGGCGACCACTTTATGAGTGTGTCGATGCGATCGGC 60  
DB 118 GATTATGAGATGACAACTGCTCATGCGCACTTATGAGAGGGGTGATGCTCTGCG 177

QY 61 ACCATGGGTGACCTGTGGGTATGGGAATTTATACGCCAAGGATGGACAGACAG 120  
 DB 178 ACATGGGGGGTCTGTGGATATGGAAATTTGTATAGCCCAAGGATGAACTATACACT 237  
 QY 121 GTGGCGGTGACACCTGGCTATTTAAACAATGATATAGTTGGTCTGTCTGGAATG 180  
 DB 238 GCAGCACTAGTACAGACTATTCACAAATGGTTAACTGTGTGCTGTGTATGAGCTC 297  
 QY 181 ACTGTTCACAAAGCACTTAATGTGCTTCGGGAACATTTAGGTCTACCTGCACCAAC 240  
 DB 298 ACTTGCACAAATGACATGATGTGTCTCCAAAGGACATTAATCTGCTACCTGCAACTAT 357  
 QY 241 TTTGGCCCTCTTACCTTGTCTCCCAACAAACATGATGGATGGTGAACCTCTCTC 300  
 DB 358 TTTTGTCTCTCGAACCCTGTCTTACCTAACAATATGTTGGTGGTCAATCTCTCTC 417  
 QY 301 CAACACTTTCAGATGGCTGAGCTGCTCTTCAAAATGCTCAATACCGAGCTGTATC 360  
 DB 418 CAACATTTTATTTAGACACAACTGCTTCTGCAAAATGCTAAATACAAAGCGGCTATC 477  
 QY 361 GTCCCGCTCTCTTGTCTAGGTACATGATGATGAAGAGGTGAGTGAATC 420  
 DB 478 GTCCCTGTATCTTTCAGAGGCTGCTGTATGAGAAAGGAGAAATAGTTTACAGTA 537  
 QY 421 AATGGCACTCATCTTCACTGCTGTTTGTATCACAACGTCGCTGAGCGAGCGACGTC 480  
 DB 538 AATGGACACATTTTCACTTGTGTTTATGATGACAAATGTTGAGAGTGTCTGATAT 597  
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 DB 598 CAATCACTTTCATTAAGGGGTCTAATATGATGATGACCAATGTCACAAATTTGGGG 657  
 QY 541 CAACACTGCAAGCAACACTATCTCAATGGCAAGGCTCTCTTCAAGTCACTCTT 600  
 DB 658 CAATATGGCAAGCAATTTCTAATGATGATGCAAGAGTCTTCAATTTGCAAGCACACA 717  
 QY 601 AGTATGATGACACCTGCTACTGCTATATCTGCTCTTCCAAATGGCAATTTGGCCAA 660  
 DB 718 AGTATGATGACACCTGCTACTGCTATATCTGCTCTTCCAAATGGCAATTTGGCCAA 777  
 QY 661 ACCATGAAGGCCCTCAAT 680  
 DB 778 ACTTGAAGGGCTCAAT 797

RESULT 14  
 AF230332 1088 bp mRNA linear PLN 26-JUN-2000  
 LOCUS Zinnia elegans expansin 2 mRNA, complete cds.  
 DEFINITION AF230332  
 ACCESSION AF230332.1 GI:7025492  
 VERSION  
 KEYWORDS  
 SOURCE Zinnia elegans.  
 ORGANISM Zinnia elegans.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; easterides II; Asterales; Asteraceae; Asteroideae;  
 Heliantheae; Zinnia.  
 1 (bases 1 to 1088)  
 Im.K.H., Cosgrove,D.J. and Jones,A.M.  
 Subcellular localization of expansin mRNA in xylem cells  
 JOURNAL Plant Physiol. 123 (2), 463-470 (2000)  
 MEDLINE 20317189  
 PUBMED 10859177  
 REFERENCE 2 (bases 1 to 1088)  
 AUTHORS Im.K.-H., Cosgrove,D.J. and Jones,A.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (02-FEB-2000) Biology, University of North Carolina,  
 Chapel Hill, NC 27599, USA  
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BASE COUNT 299 a 205 c 237 g 347 t  
 ORIGIN

Query Match 60.1%; Score 409.6; DB 8; Length 1088;  
 Best Local Similarity 75.1%; Pred. No. 4,7e-115;  
 Matches 511; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 1 GACTACGGTGGCTGGAGAGCGGCCACGCTTTATATGATGGTGTGACGACTTGGC 60  
 DB 70 GCTATGGAGGTGGGAAATATGCTATCCACTTTTACGGTGGGAGATGCCCTGGA 129  
 QY 61 ACCATGGGTGAGCTTGTGGATATGGAATTTATACAGCCAAAGGATGAGCAAGACG 120  
 DB 130 ACAATGGGTGGTGTGTGATATGAAATCTGTATAGCAAGATATGCACTTACACT 189  
 QY 121 GTGGGCTGACGACGCTGCTATTTAACAATGATTAAGTTGTGTGCTTGTGGAATG 180  
 DB 190 GGGGCACTTGTAGTACGCTTCTTCAACAATGAGTTAAGTTGGGTGATGTAGAGATG 249  
 QY 181 ACTTGTACAAAGCACTTAATGATGCTTCCGGAACTATTAAGGTCTACGCCAACAC 240  
 DB 250 AGATCAACAGCAAGCCCTTAATATGATGCTGCGGCTTAATATGTTGATGCGCAACAA 309  
 QY 241 TTTTGGCTCTTAACTTGTCTCTCCCTAACAACAATGATGATGGTGGCAACCTCTCTC 300  
 DB 310 TTTTGGCCACTTAACTTGTCTTGTCTAACAAGATGATGGTGGTGGCAACCTCTCTC 369  
 QY 301 CAACACTTGCACATGCTGAGCTGCTCTCTTCAATGCTCAATACCGACTGTATC 360  
 DB 370 CAACATTTTGTATGATGACAGAACCTCTCTTCTGCAAAATGACAAATATATGAGCTGGAATT 429  
 QY 361 GTCCCGCTCTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
 DB 430 GTCCCTATATCTTCAAGAGGCTCCATGCTGCTCAAGAAAGAGAGATGATTTACTATA 489  
 QY 421 AATGGCACTCATCTTCACTGCTGTTTGTATCACAACGTCGCTGAGCGAGCGACTC 480  
 DB 490 AATGGTCACTTCACTTCACTTGAATTTGATCACAACGTCGAGGAGGATGTT 549  
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 DB 550 CACTCATGTTCATTAAGGATCAAAACCGGGTGGCAATCATGTCTAAGAAATTTGGGGC 609  
 QY 541 CAACACTGCAAGCAACAACTATCTCAATGATGATGATGATGATGATGATGATGATGAT 600  
 DB 610 CAACACTGCAAGCAACAACTATCTTCAAGCTCAACAGCTATCTTCAGAGTCAAGCT 669  
 QY 601 AGTATGATGACACCTGCTACTGCTATATCTGCTCTTCCAAATGGCAATTTGGCCAA 660  
 DB 670 AGTATGATGACACCACTCATCTTCAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCT 729  
 QY 661 ACCATGAAGGCCCTCAAT 680  
 DB 730 ACTTCCAAAGGGGACCAAT 749

RESULT 15  
 AB029083 1220 bp mRNA linear PLN 19-JUN-2001  
 LOCUS Prunus persica PpExp1 mRNA for expansin, complete cds.  
 DEFINITION AB029083  
 ACCESSION AB029083.1 GI:11907553  
 VERSION  
 KEYWORDS expansin.



SOURCE Prunus persica ripening fruit cDNA to mRNA.  
ORGANISM Prunus persica  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
REFERENCE 1 (sites)  
AUTHORS Hayama, H.  
TITLE Homolog to expansin in peach fruit  
JOURNAL Published Only in Database (2000) In press  
REFERENCE 2 (bases 1 to 1220)  
AUTHORS Hayama, H.  
TITLE Direct Submission  
JOURNAL Submitted (18-JUN-1999) Hiroko Hayama, National Institute of Fruit  
Tree Science, Department of Pomology; 2-1 Fujimoto, Tsukuba,  
Ibaraki 305-8605, Japan (E-mail: hiroko@fruit.affrc.go.jp,  
Tel:+81-298-38-6502, Fax:+81-298-38-6437)  
FEATURES  
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BASE COUNT 323 a 249 c 302 g 346 t  
ORIGIN  
Query Match 60.1%; Score 409.4; DB 8; Length 1220;  
Best Local Similarity 76.4%; Pred. No. 5.5e-115;  
Matches 516; Conservative 0; Mismatches 156; Indels 3; Gaps 1;  
QY 7 GGTGGCTGCAGAGCGGCCACGACCTTTTATGTGTGTGACGATCTGGACCATG 66  
DB 136 GGAGGTGCTTGATGAAATTTGTATAGCCAAAGGTATGAAACCACTGCAGCT 195  
QY 67 GGTGGAGCTTGTGGGATGGGAATTTATAGCCAAAGGTATGCAAGCAACGTTGGC 126  
DB 196 GGAGGTGCTTGATGAAATTTGTATAGCCAAAGGTATGAAACCACTGCAGCT 255  
QY 127 CTGAGCACTGCGCTATTTAACAATGATTAAGTTGTGTGTGCTTCCGAATGACTTGT 186  
DB 256 CTGAGCACTGCGCTATTTAACAATGATTAAGTTGTGTGTGCTTCCGAATGACTTGT 315  
QY 187 ACAACGACCTTAATGTGTGCTTCCGGGAACTATTAGGCTCATGTCACCACTTTTGC 246  
DB 316 GACAGTGACCCCAATGTGTGCTTCCGGGAACTATTAGGCTCATGTCACCACTTTTGC 375  
QY 247 CCTGCTAATGCTCTCCCTAAACAATGATGATGGTGAACCTCTCTCCAACAC 306  
DB 376 CCTGCTAATGCTCTCCCTAAACAATGATGATGGTGAACCTCTCTCCAACAC 435  
QY 307 TTGACATGGCTGAGCTGCTCTCTCAATGCTCAATACCGAGCTGTATGTCCTCC 366  
DB 436 TTGATTTGGCTGAGCTGCTCTCTCAATGCTCAATACCGAGCTGTATGTCCTCC 495  
QY 367 GTTCCTTTCTGAGGTATGATGAAGAAAGGTGAGTGAAGTTTACATCAATGAGC 426  
DB 496 GTTCCTTTCTGAGGTATGATGAAGAAAGGTGAGTGAAGTTTACATCAATGAGC 555  
QY 427 CACTCATACCTCAACCTCGTTTGTATCAAAAGTGTGGGCGAGGGAGCTCCACTCT 486  
DB 556 CACTCATACCTCAACCTCGTTTGTATCAAAAGTGTGGGCGAGGGAGTGTGCACTCT 615

QY 487 GTTCGATMAAGGGGTCTCGAAGTGTGATGCAATTCATGCTAGAAATTGGGCCAAAC 546  
DB 616 GTTCAATCAAGGGGTCTCGAAGTGTGATGCAATTCATGCTAGAAATTGGGCCAAAC 675  
QY 547 TGGCAAGCAACACTATCTCAATGCGCAAGGCTTTCCTTTCAAGTCACTCTTAGTGT 606  
DB 676 TGGCAGACCAACTCTTACCTCAATGCGCAAGGCTTTCCTTTCAAGTCACTCTTAGTGT 735  
QY 607 GGTGCACTTCACCTGCTATTAATCTGTTCTTCCAAATGGCAATTTGGCCAAACCTAT 666  
DB 736 GTTGAAGTGTGA--CCAGCAATGCTGTGCAAGTGTGCAAGTGTGCAAGTGT 792  
QY 667 GAAGGCCCTCAATTC 681  
DB 793 TCGGGGCTCAATTC 807

Search completed: October 13, 2002, 23:33:48  
Job time : 1815 secs



STIC-Biotech/ChemLib

77634

From: Saidha, Tekchand  
Sent: Wednesday, October 09, 2002 5:40 PM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search request - 09/896301

09/896301

Please search the data base & interference files :

SEQ ID NO : 1 through 7

Thank you !

*Tekchand Saidha*  
*Primary Examiner*  
*Art Unit 1652, CM1, Room No. 10D05*  
*Mail Box 40601*  
*(703) 305-6595*

10D01

Point of Contact  
P. Sheppard  
Telephone number: (703) 308-4499

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: 10/16/02  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
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AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
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WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

